

FIGURE 1

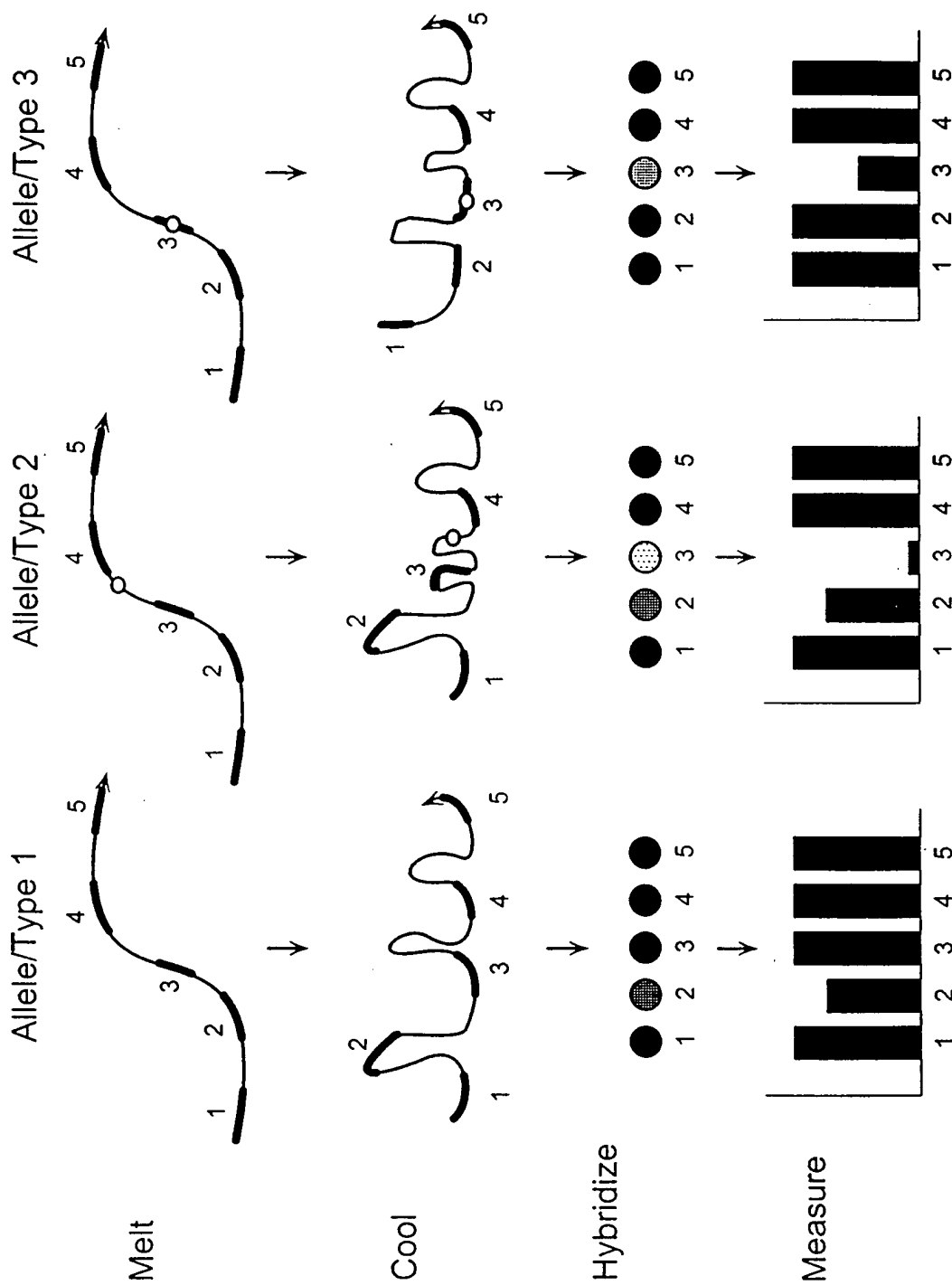


FIGURE 2

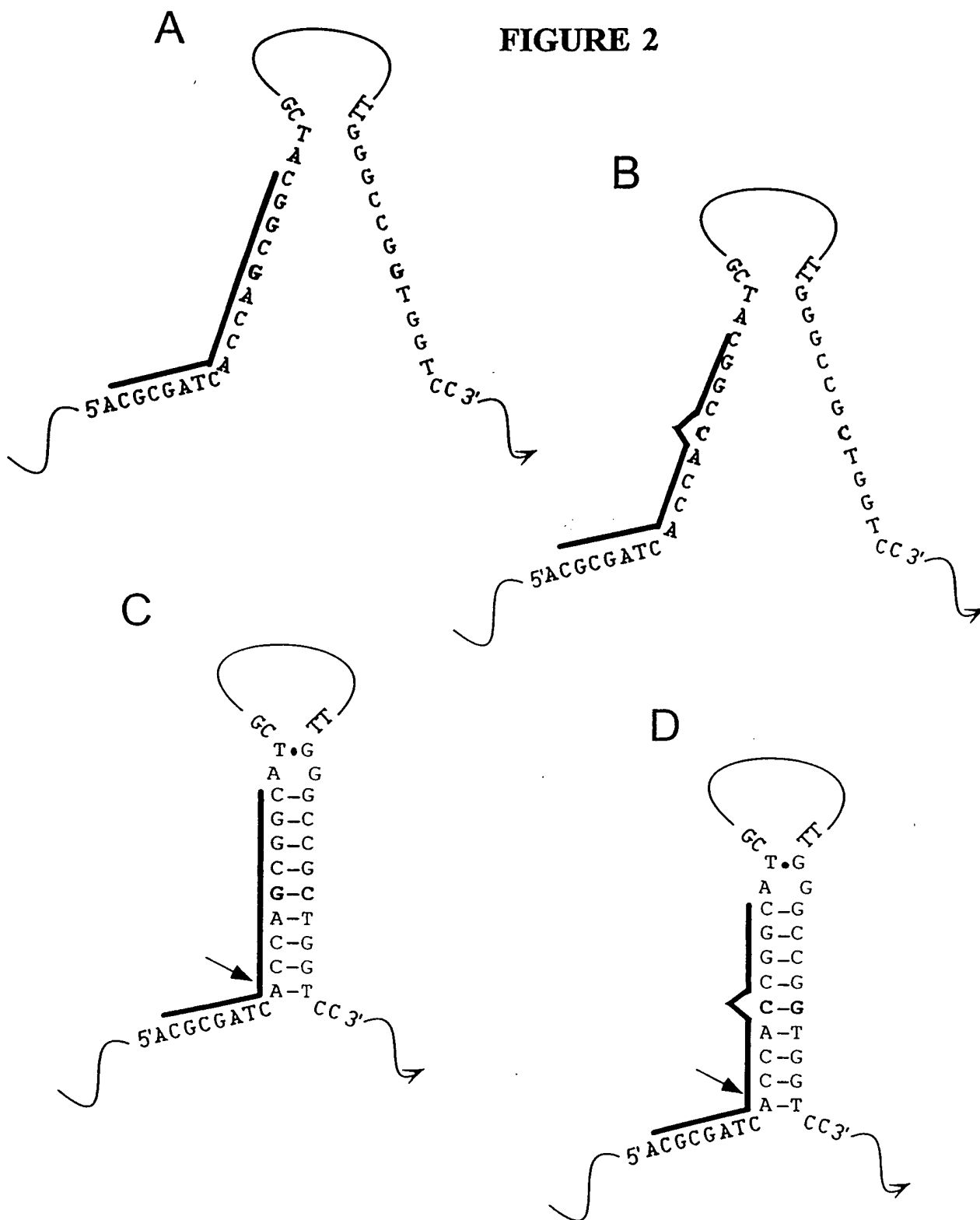


FIGURE 3

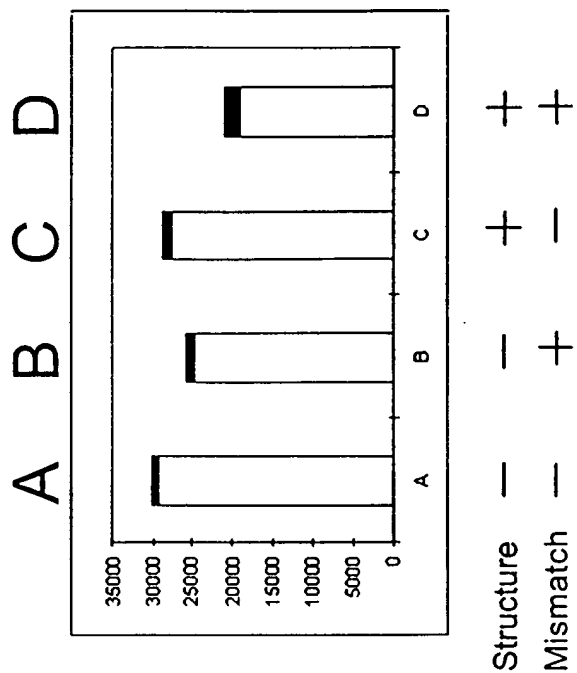
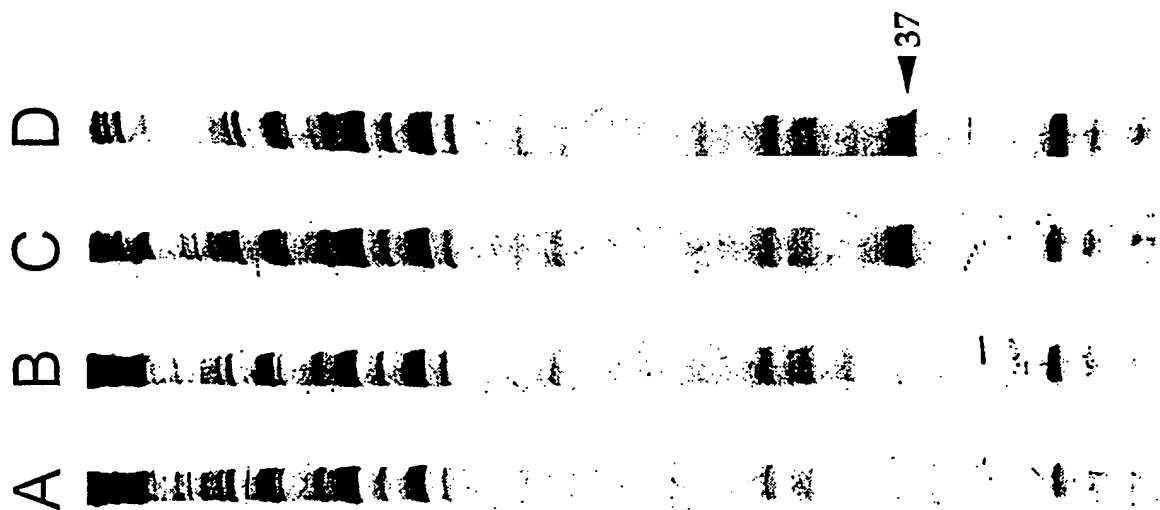


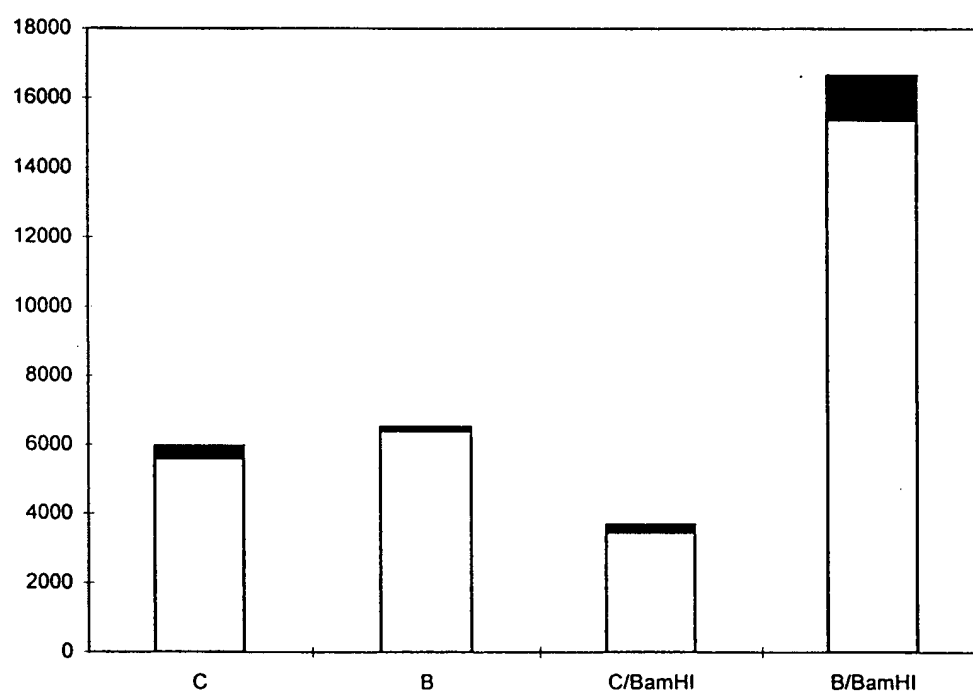
FIGURE 4

FIGURE 5

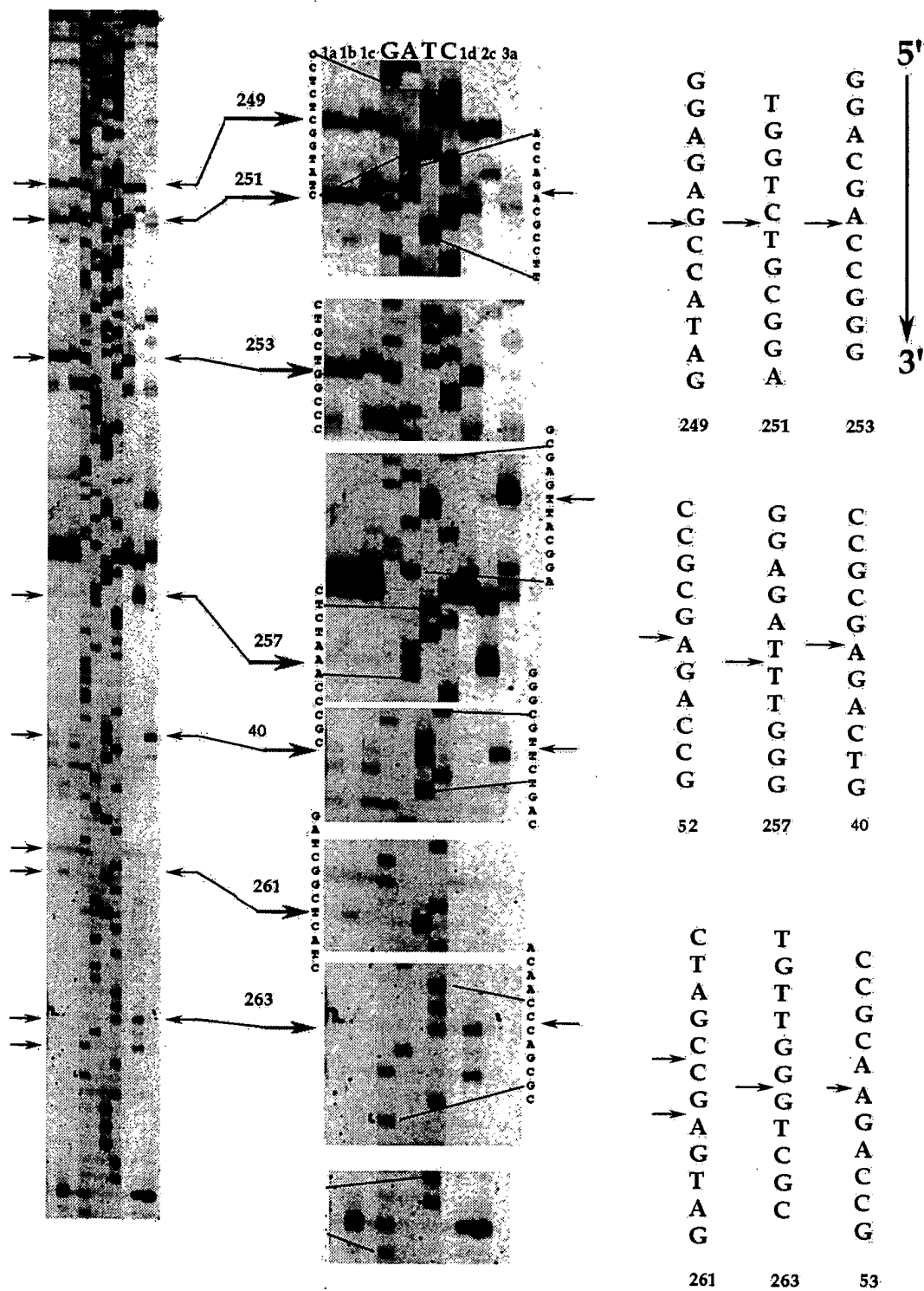


FIGURE 6

Consensus:GATTCGTCT TCACGCAGAA AGCGTCTAGC CATGGCGTTA GTATGAGTGT CGTGCAGCCT					
HCV 1a	-----	-----	-----	-----	-----
HCV 1b	-----	-----	-----	-----	-----
HCV 2c	-----	-----	-----	-----	--A-
HCV 3a	-----	-C-----	-----	-C-----	-----
	#249	#251			
CCAGGACCCC	<u>CCCTCCCGG AGAGCCATAG</u>	<u>TGGTCTGCCG AACCGGTGAG</u>	TACACC GGAA		
-----	-----	-----	-----		
-T-----	-----	-----	-----		
-C-----	-----	-----	-----		
-----	-A-----	-----	-----		
#253	#257				
TTGCCAGGAC	<u>GACCGGGTCC TTTCTTGGAT</u>	CAACCCGCTC	AATGCCCTGA	<u>GATTGGGCG</u>	
-----	-----	-----	-----	-----	
-----	-----	-----	-----	-----	
-G--A-T-	-----	A--A--	T--C-C	C--	
-C-TG-GT-	-----	-G-----	--A-CA-	A--	
#40	#261	#263			
TGCCCCCGCA	<u>AGACTGCTAG CCGAGTAGTG</u>	<u>TTGGGTCCGG</u>	AAAGGCCCTTG	TGGTACTGCC	
-----	-----	-----	-----	-----	
-----G	-----	-----	-----	-----	
-----	-----C-	-T-----	-----	-----	
-----G	-TCA-----	-----	-----	-----	
TGATAGGGTG	CTTGGGAGTG	CCCCGGGAGG	TCTCGTAGAC	CGTGCAATC	
-----	-----	-----	-----	-----	
-----	-----	-----	-----	-----	
-----	-----A	-----	-----	-----	

FIGURE 7

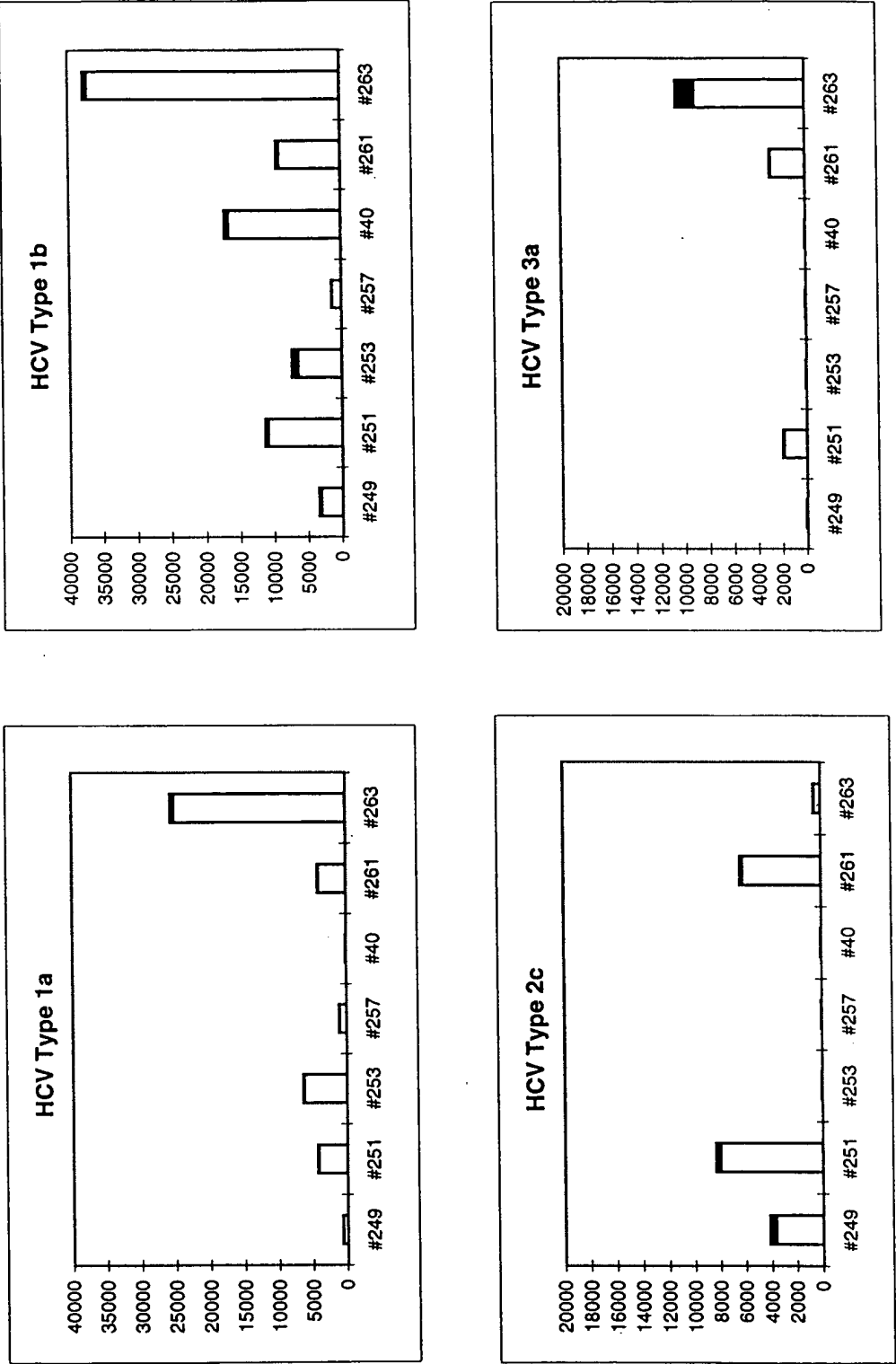


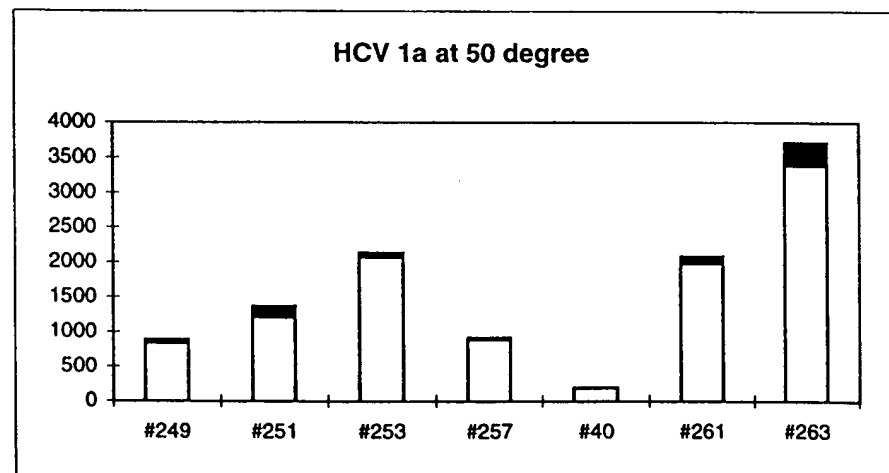
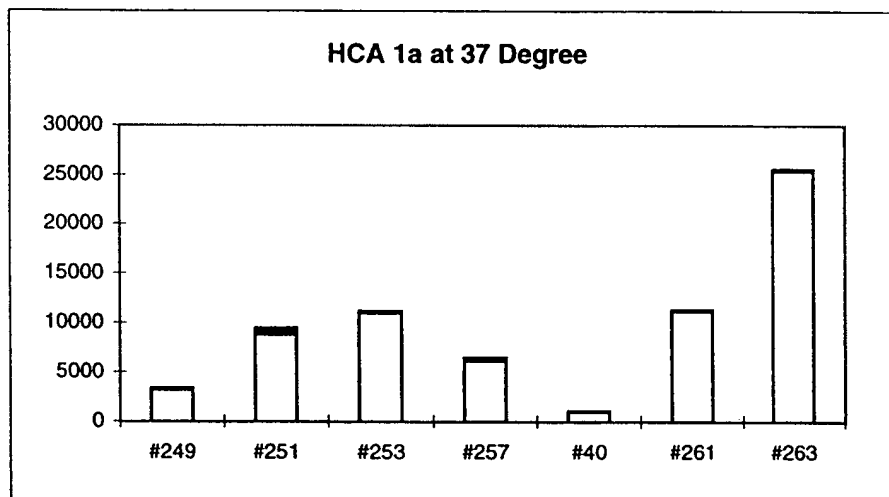
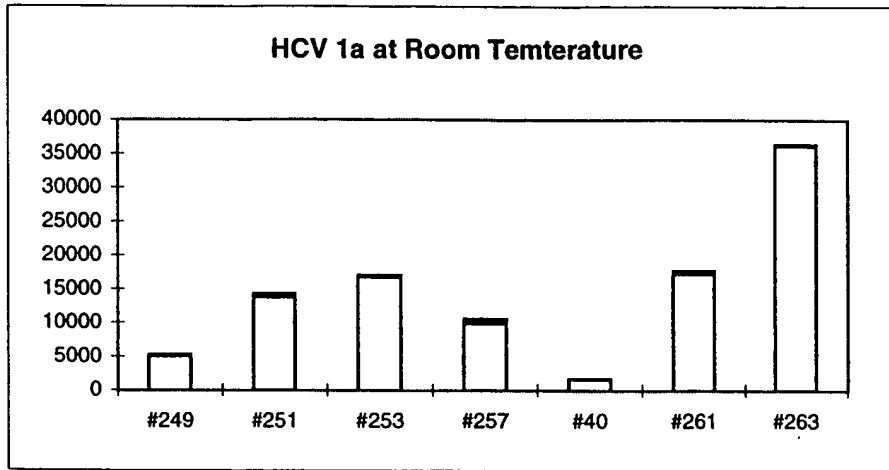
FIGURE 8A

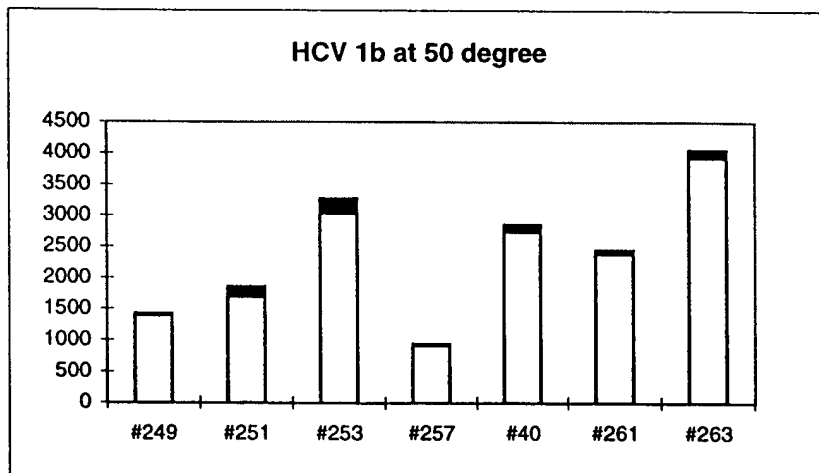
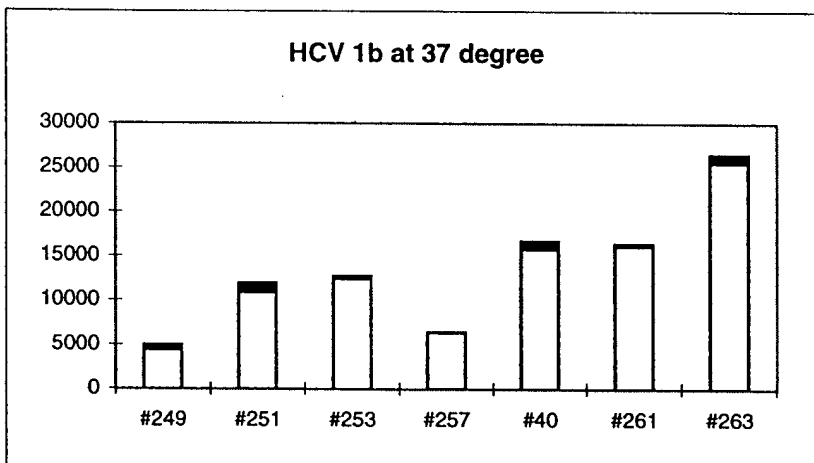
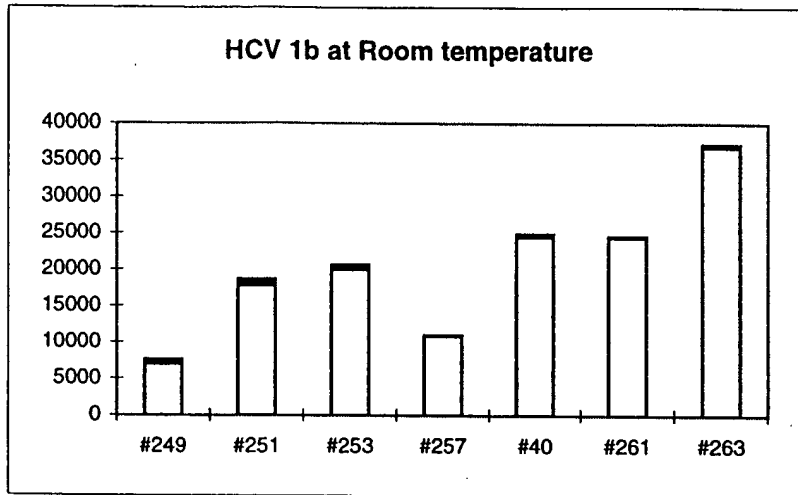
FIGURE 8B

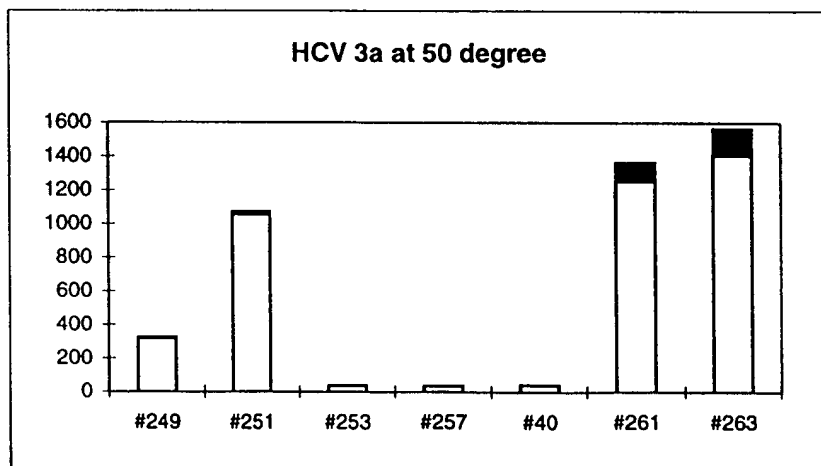
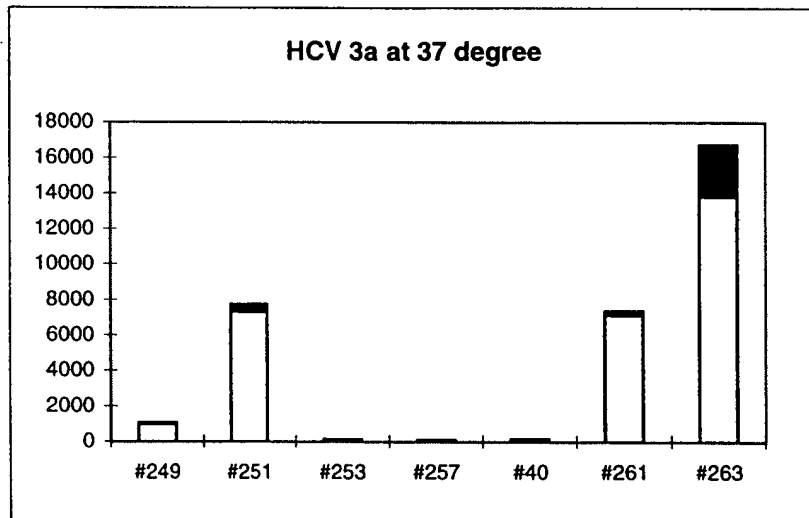
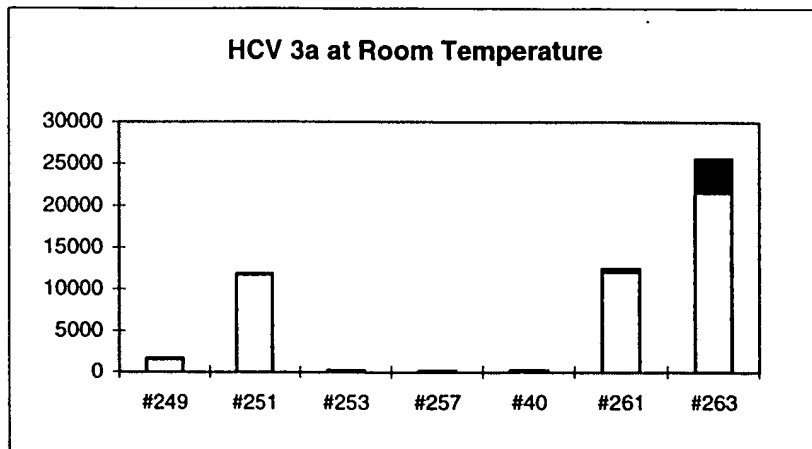
FIGURE 8C

FIGURE 9A

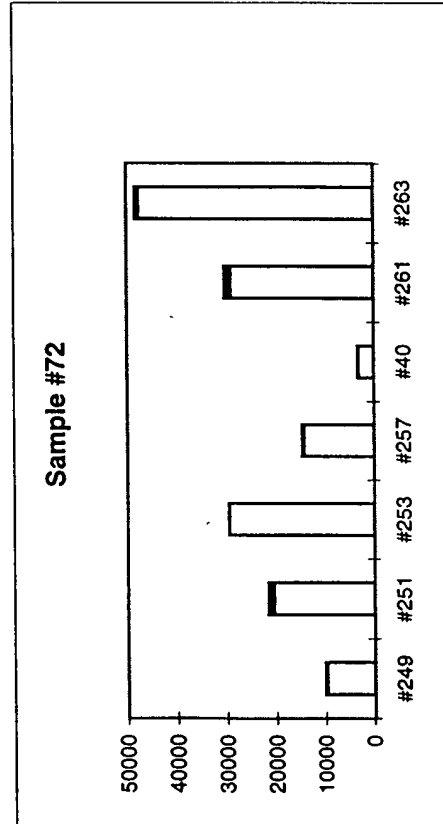
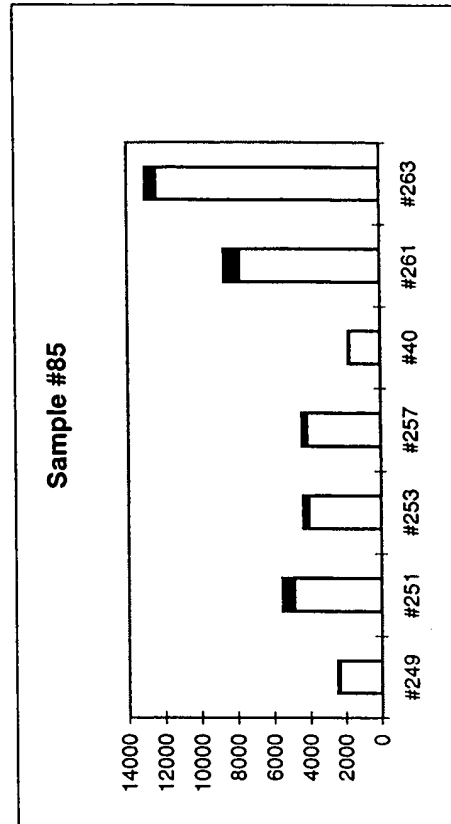
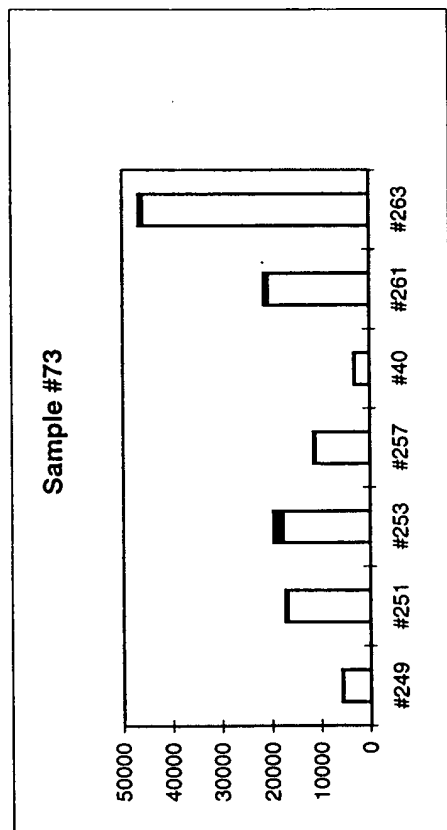
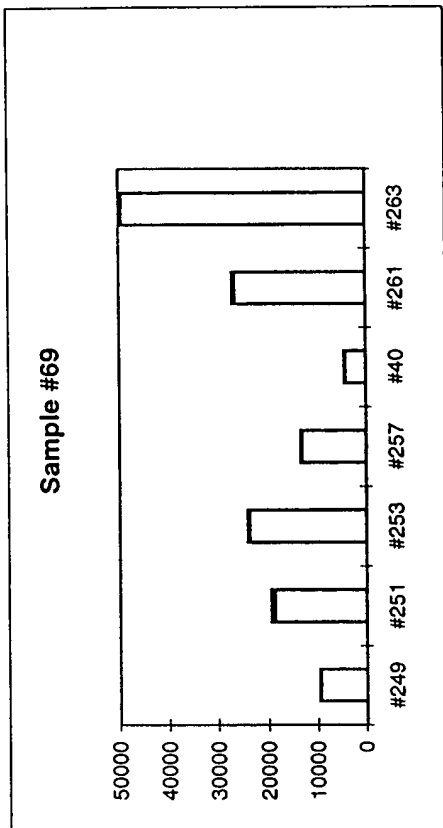


FIGURE 9B

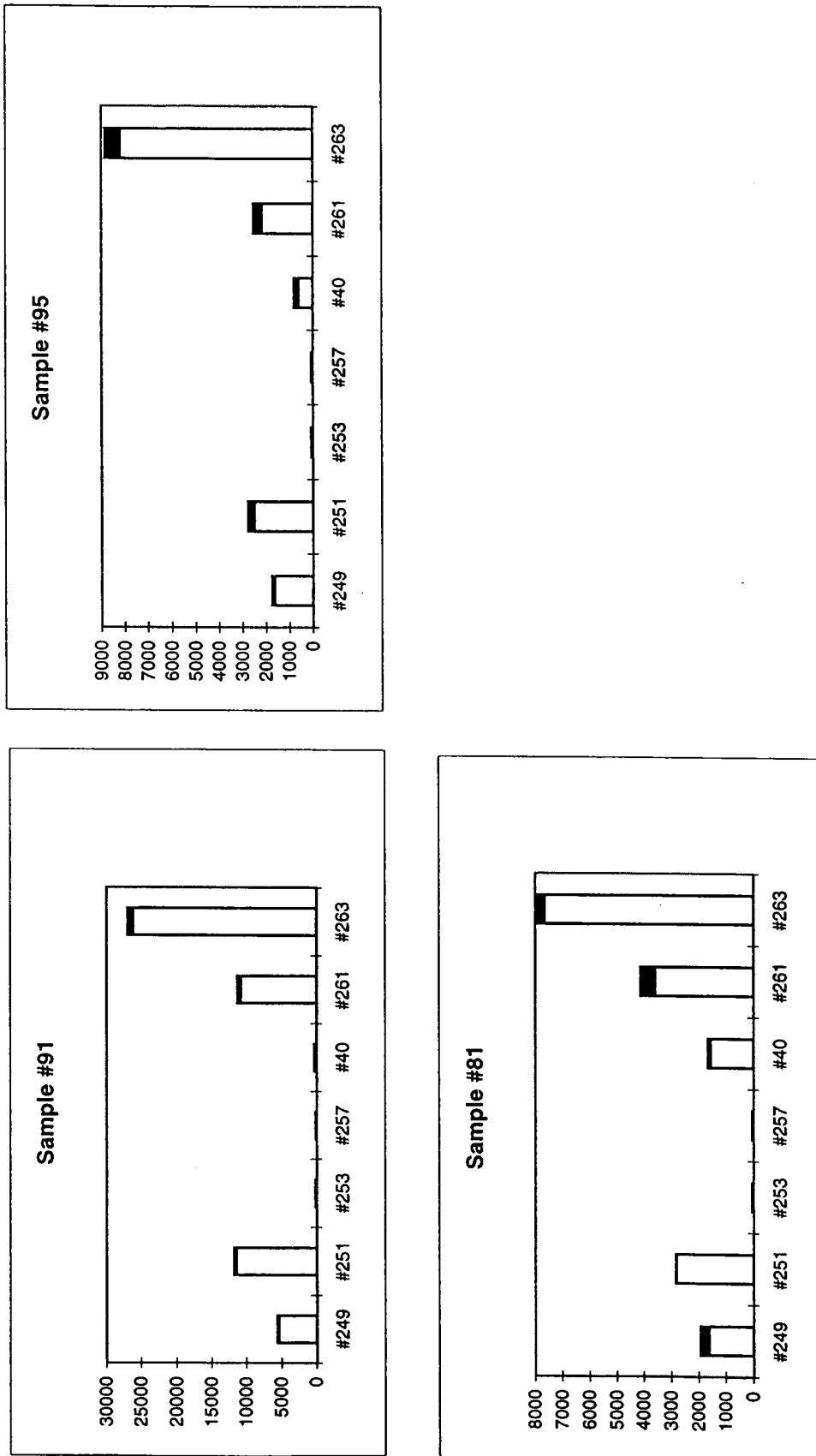


FIGURE 9C

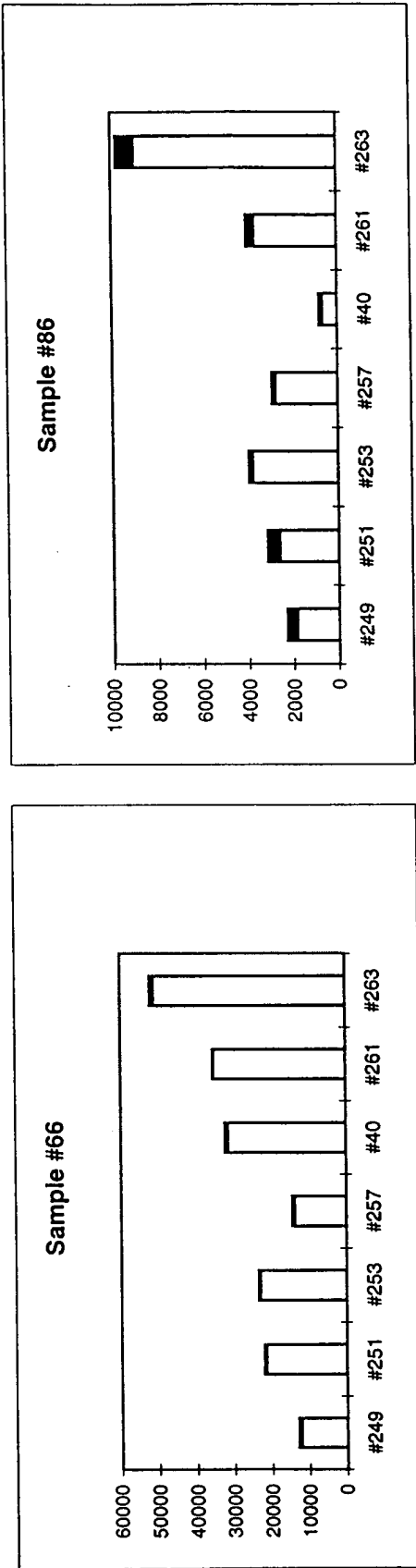


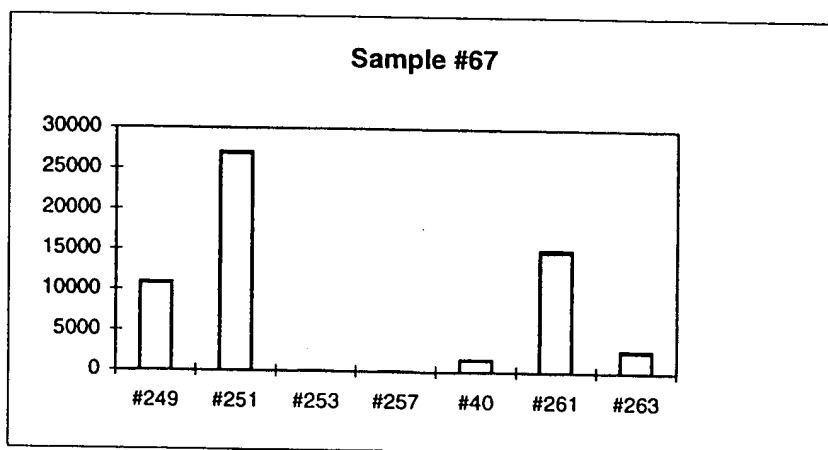
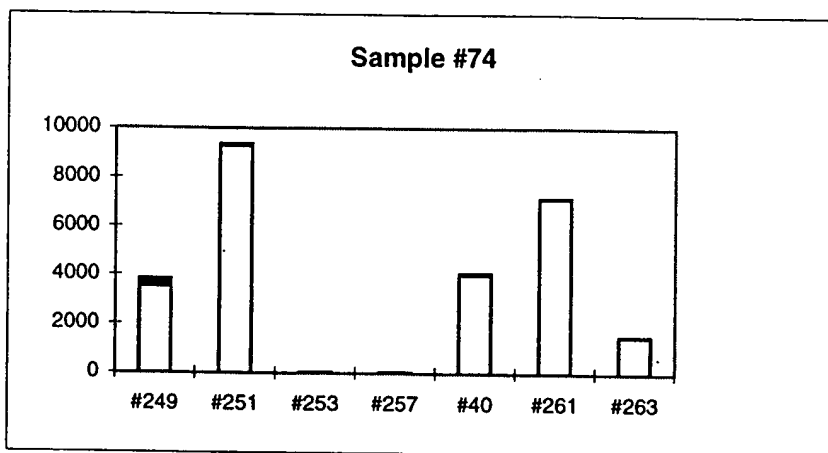
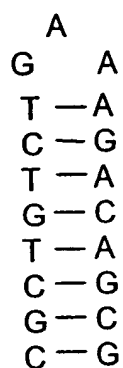
FIGURE 9D

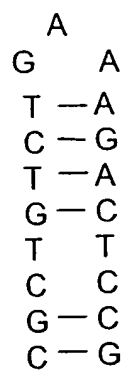
FIGURE 10

#80



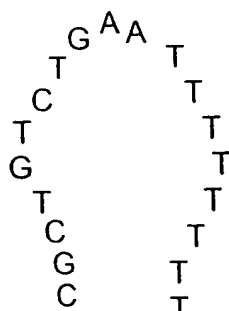
5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#81



5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

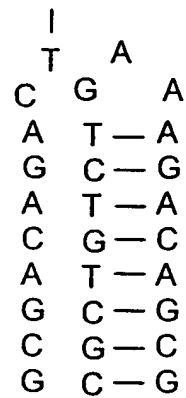
#82



5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

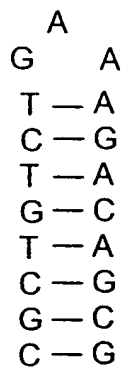
FIGURE 11A

#2) 5' Biotin



#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#FD91) 3' Biotin - CGAGAGACCA-5'



#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'



#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT -5'

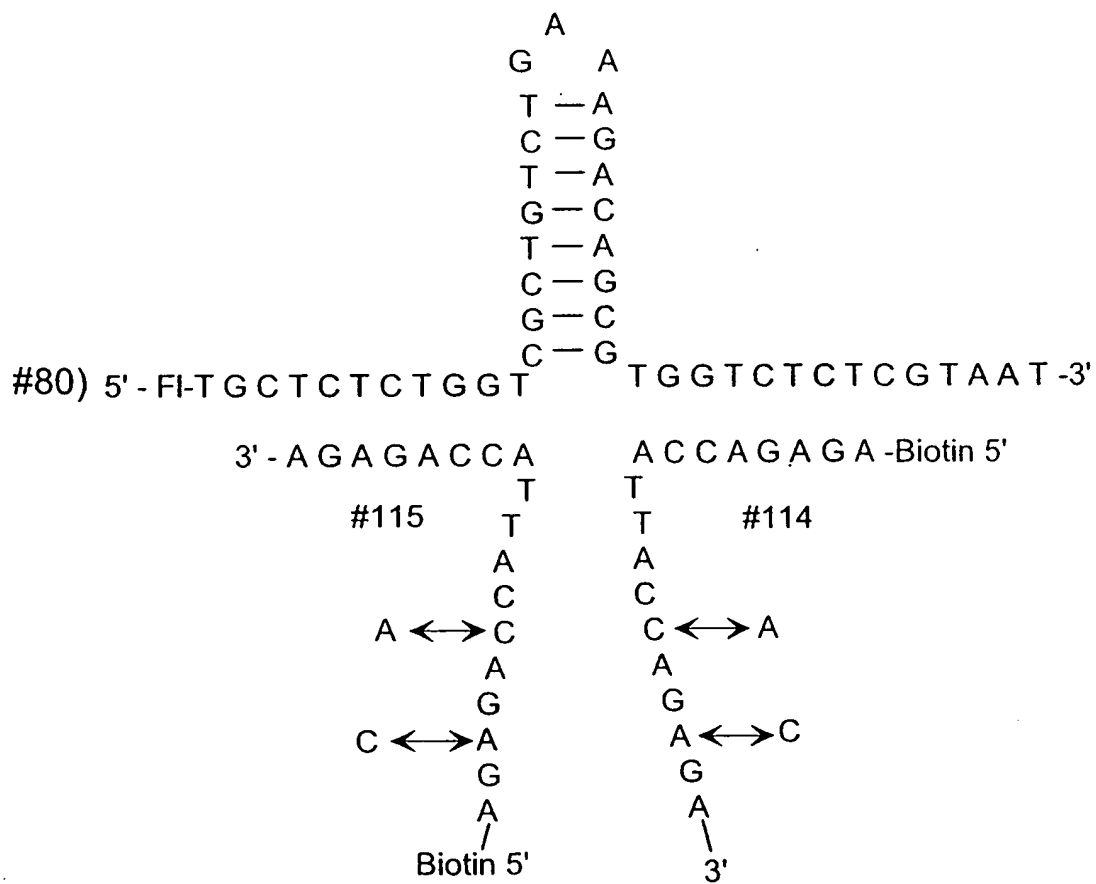
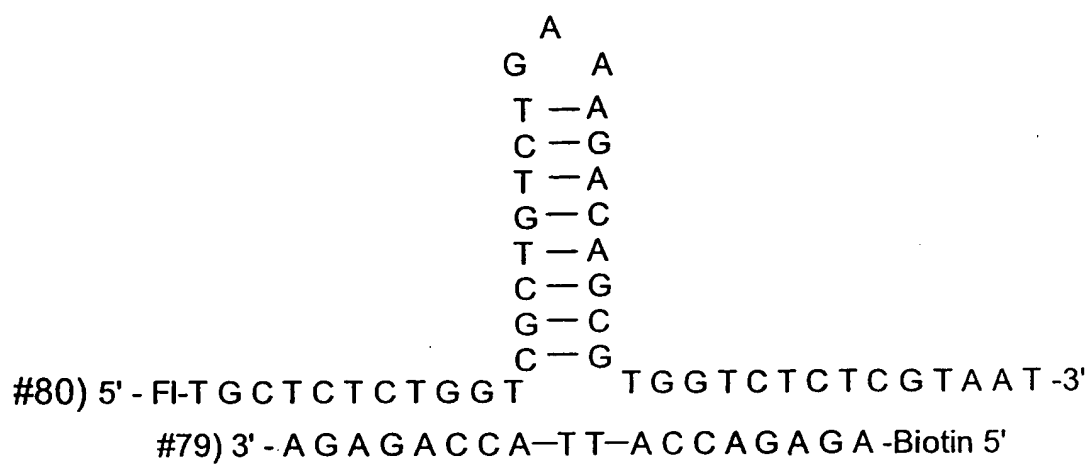
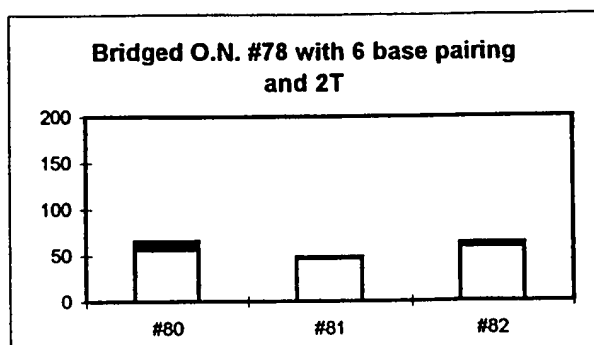
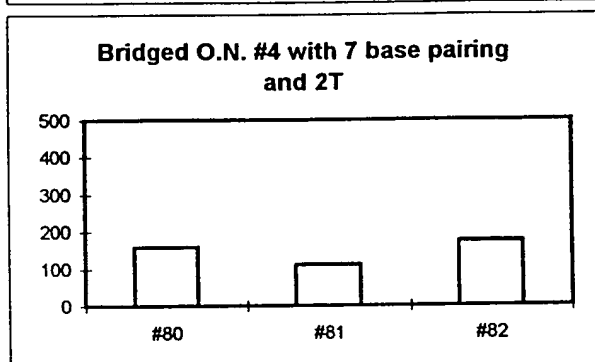
FIGURE 11B

FIGURE 12

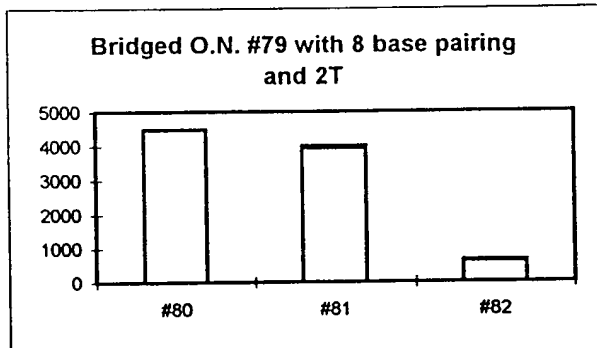
A



B



C



D

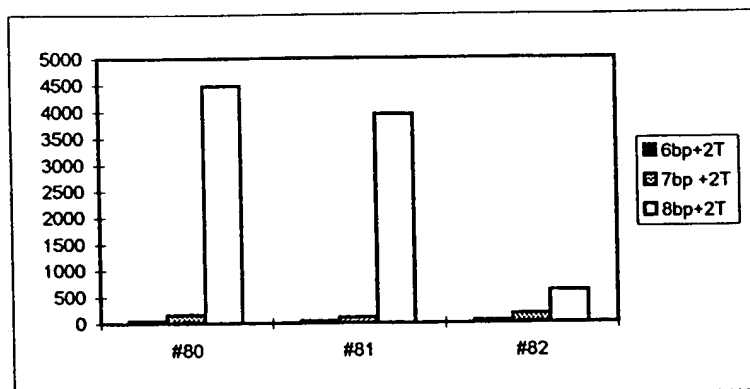


FIGURE 13A

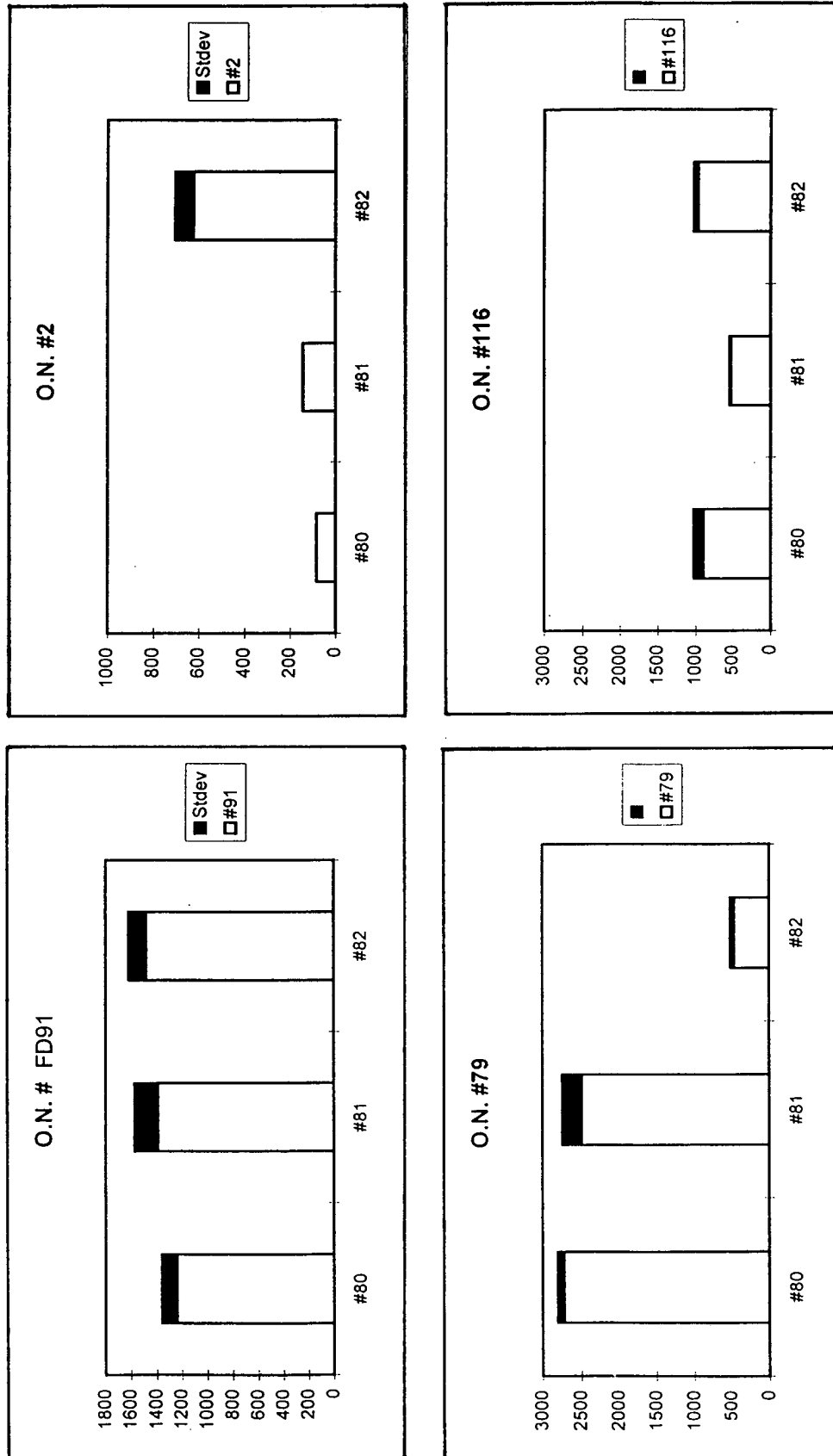


FIGURE 13B

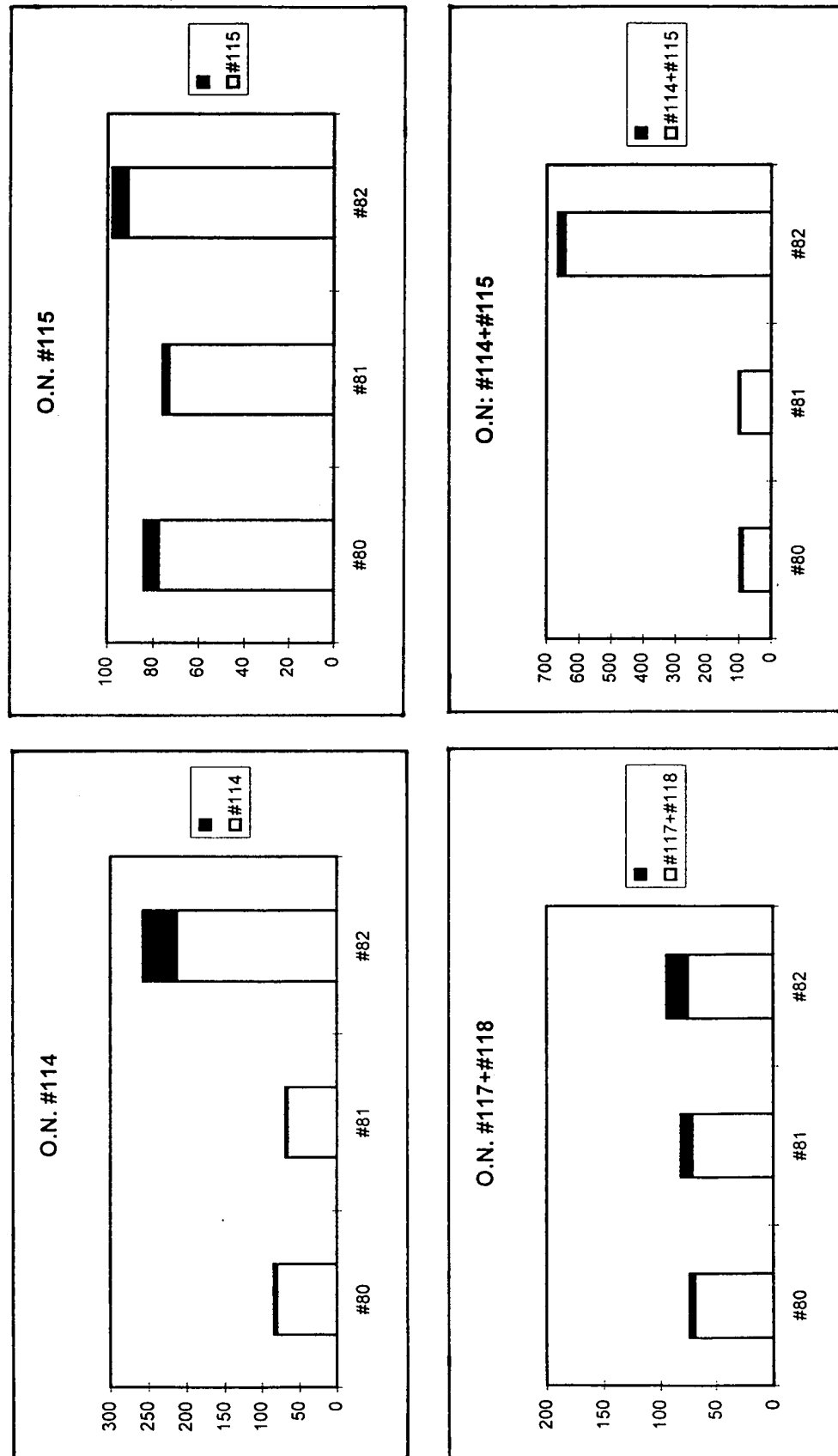


FIGURE 14

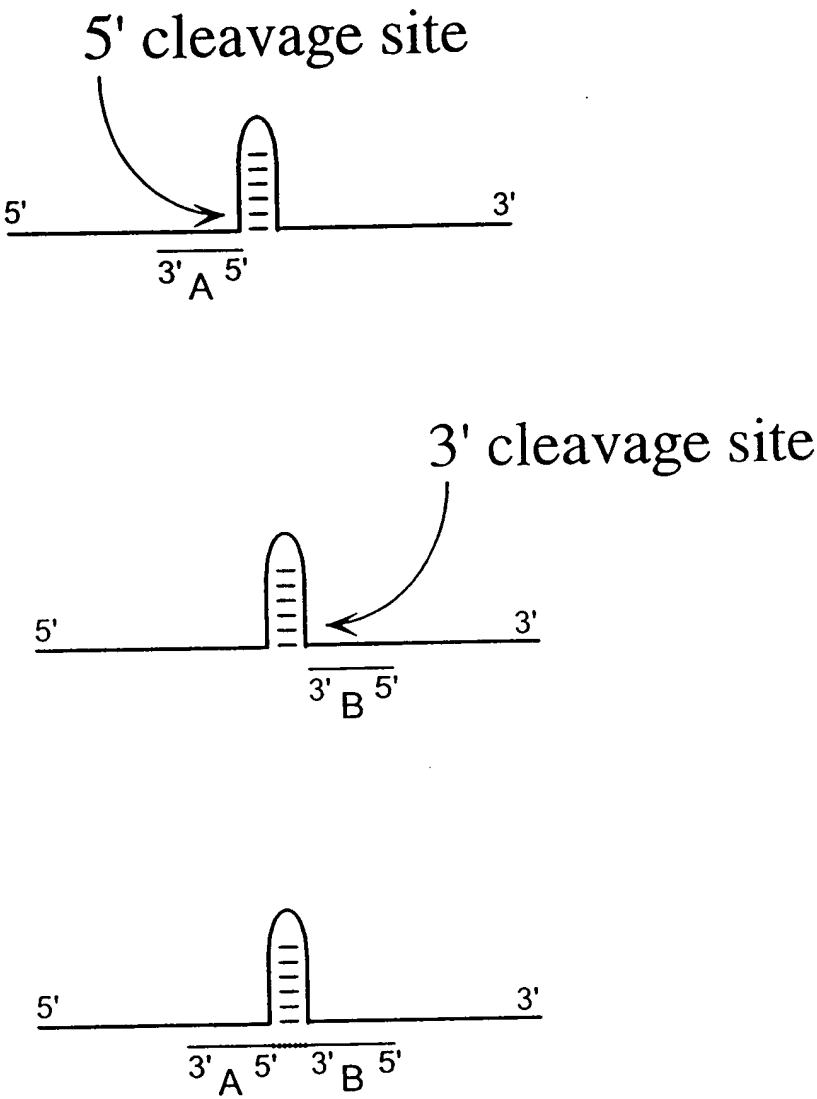


FIGURE 15

[illegible]

FIGURE 16A

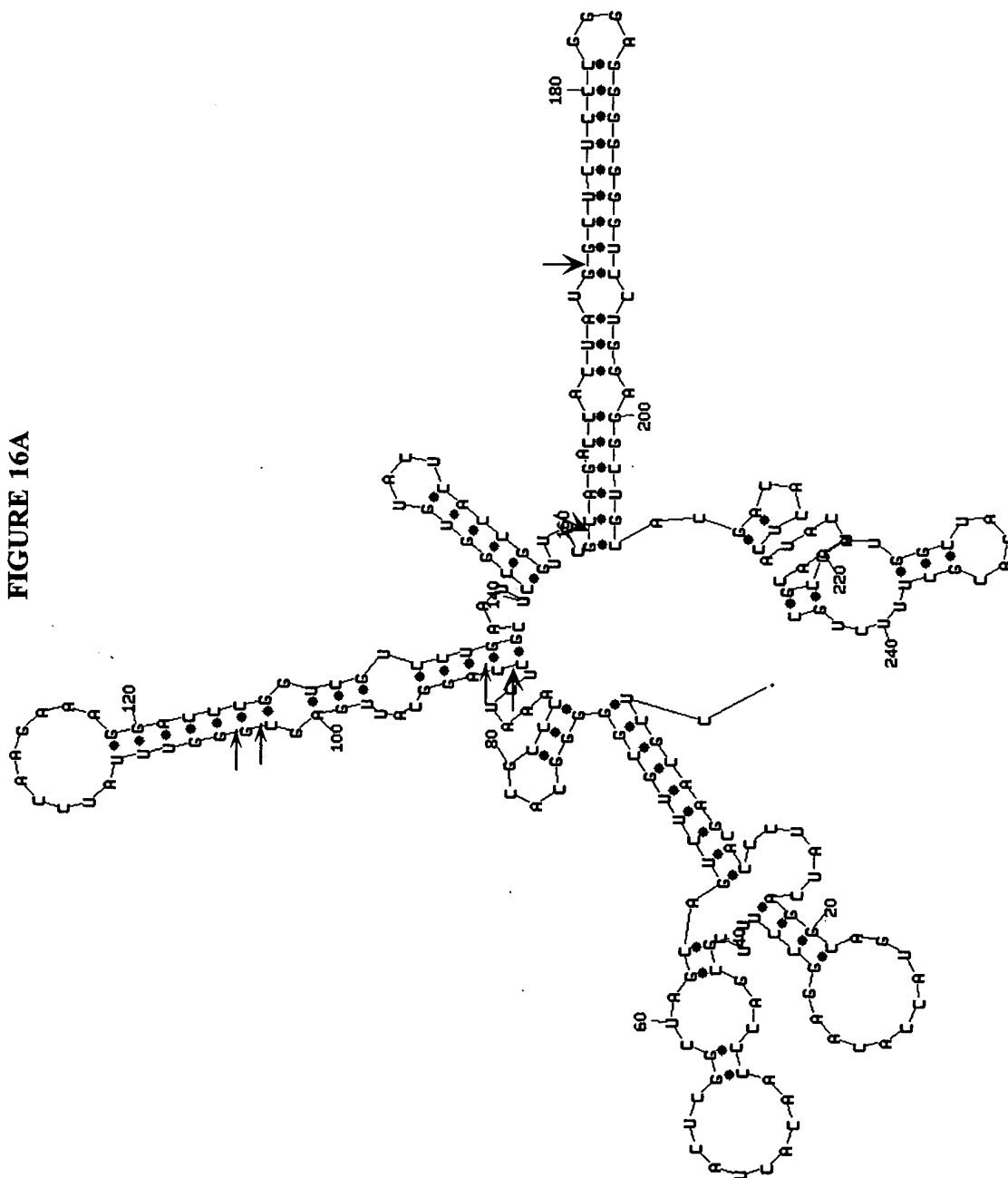


FIGURE 16B

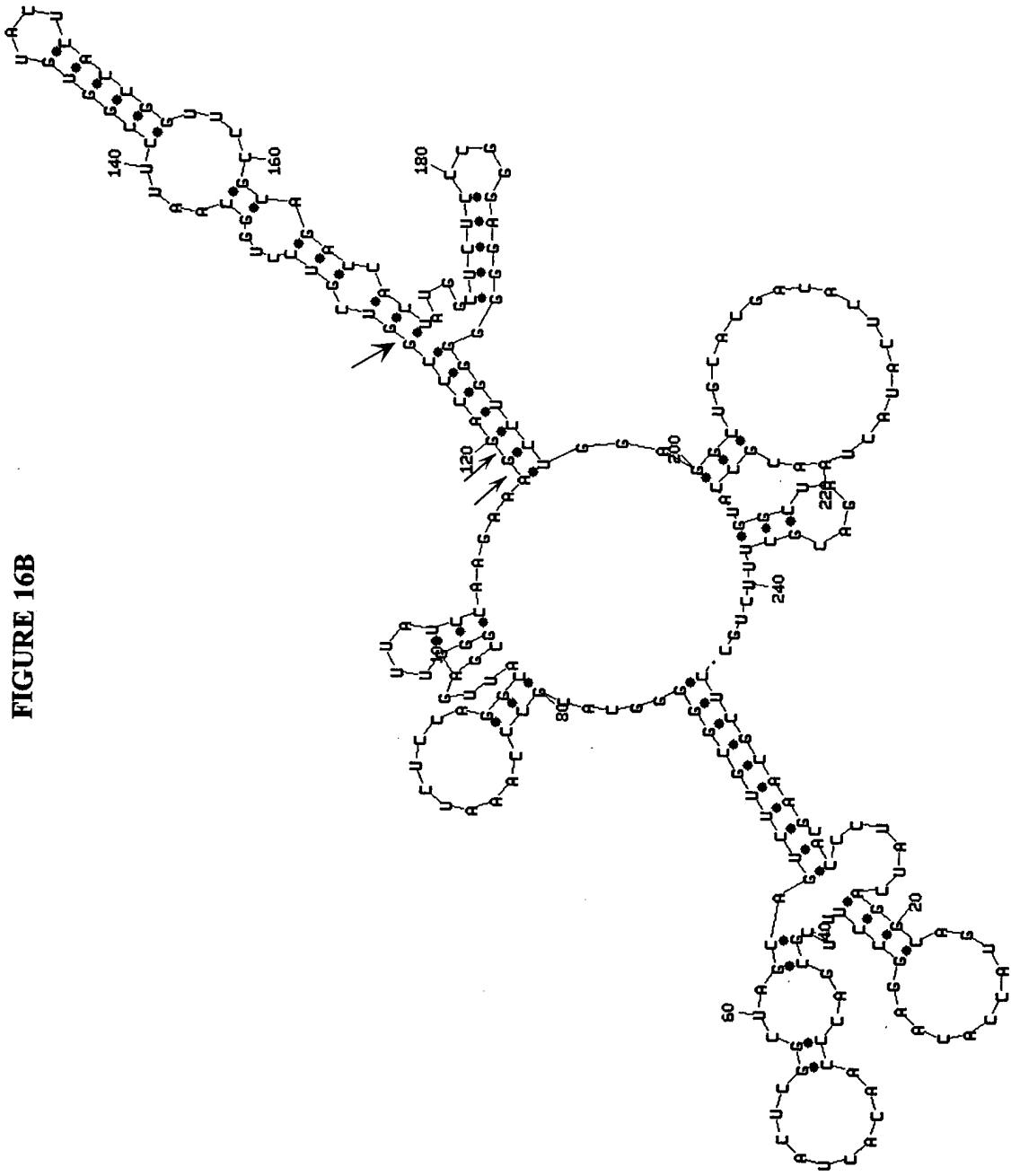


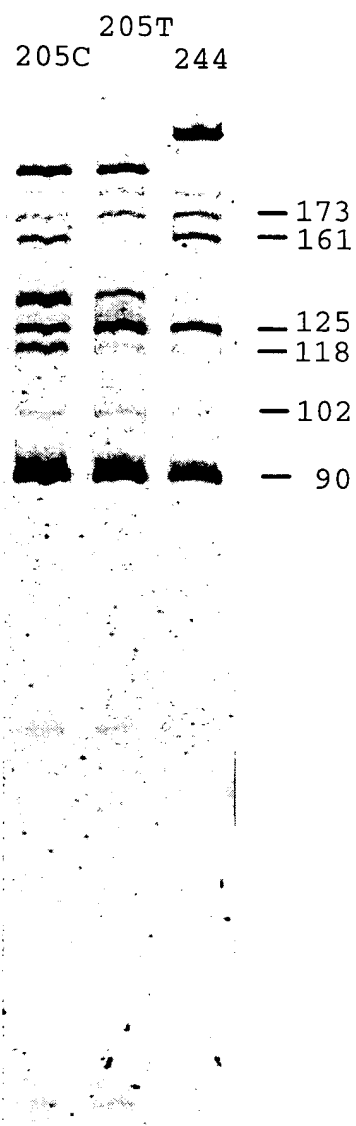
FIGURE 17A

FIGURE 17B

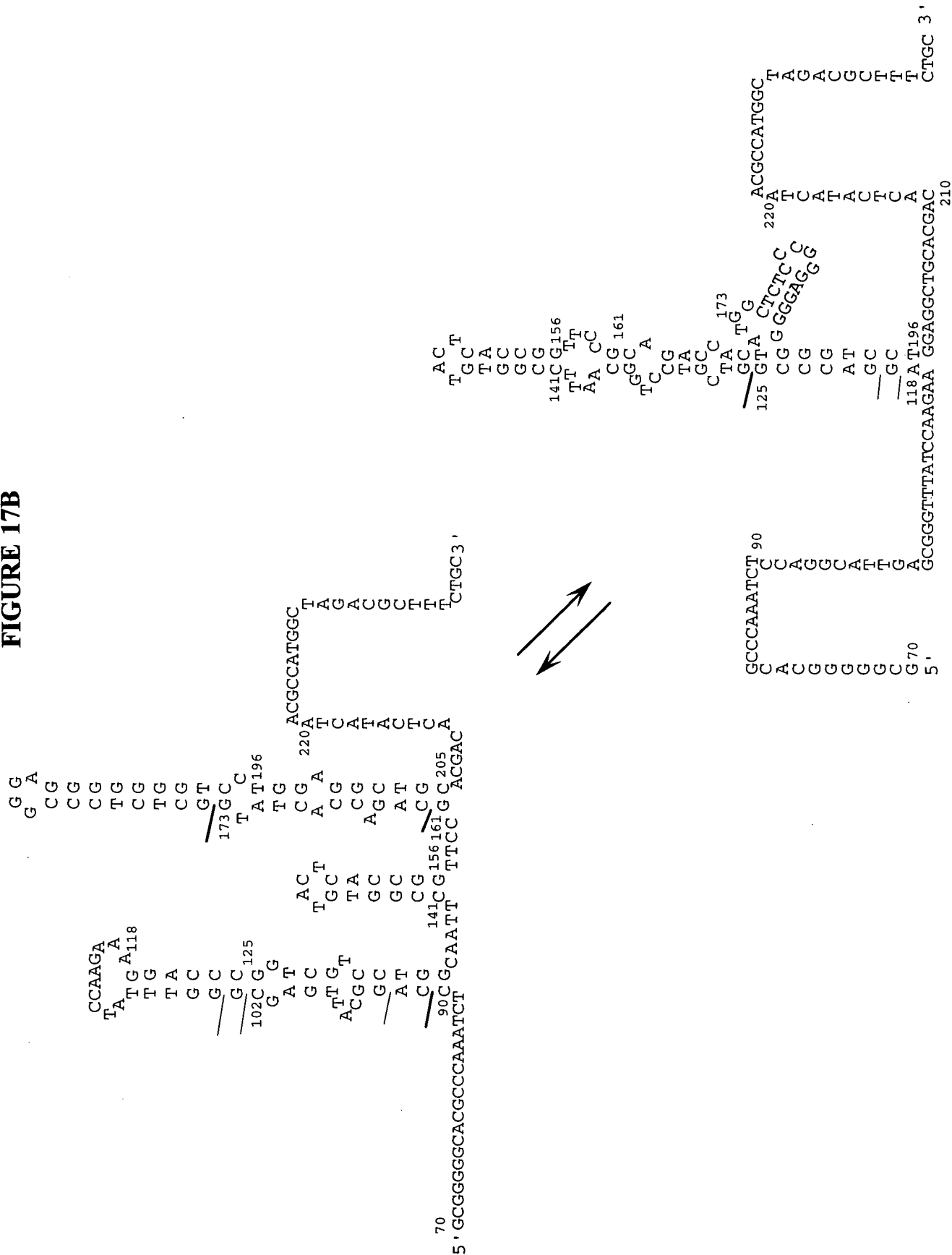


FIGURE 17C



FIGURE 18A

HCV 1a

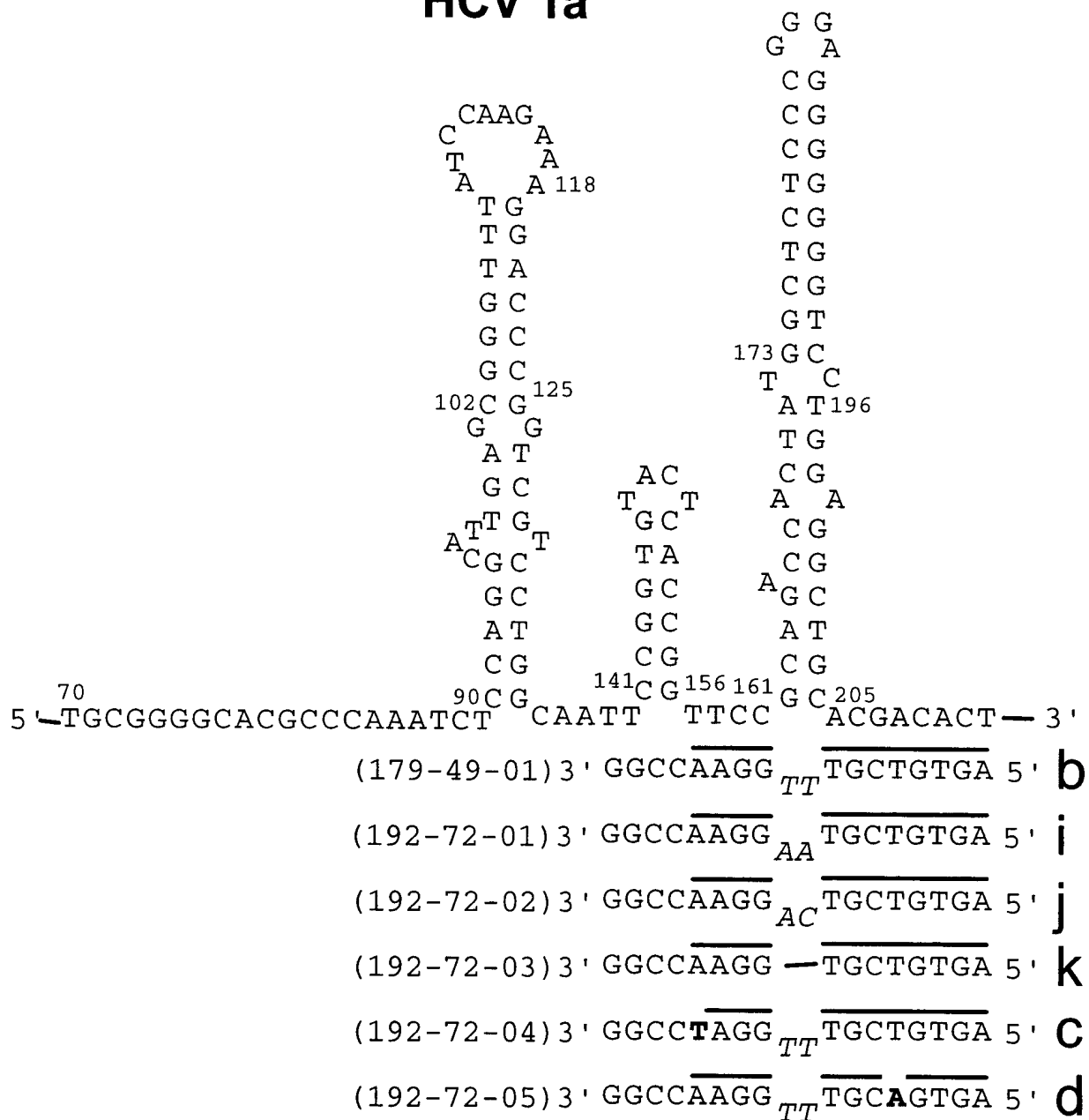


FIGURE 18B

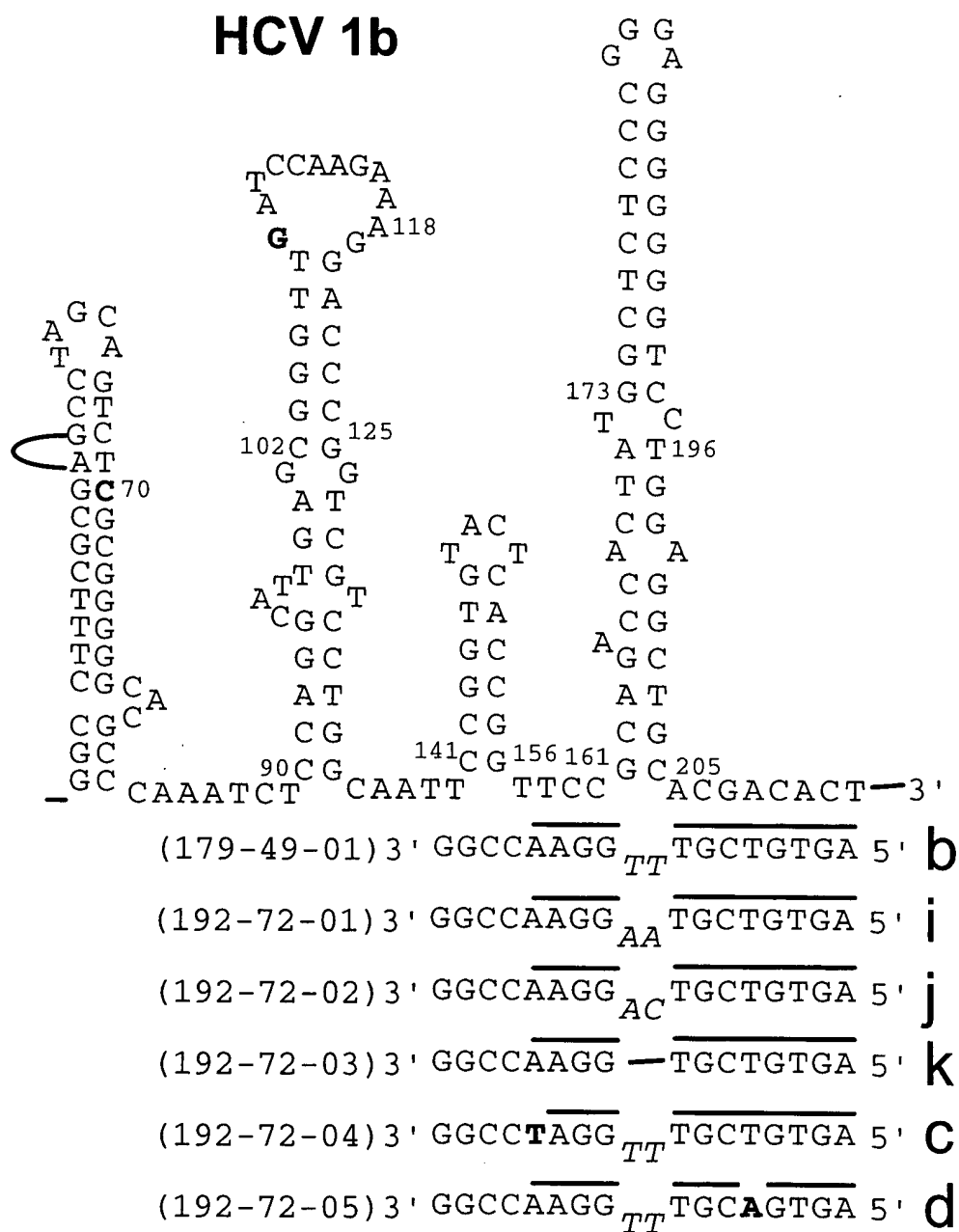


FIGURE 18C

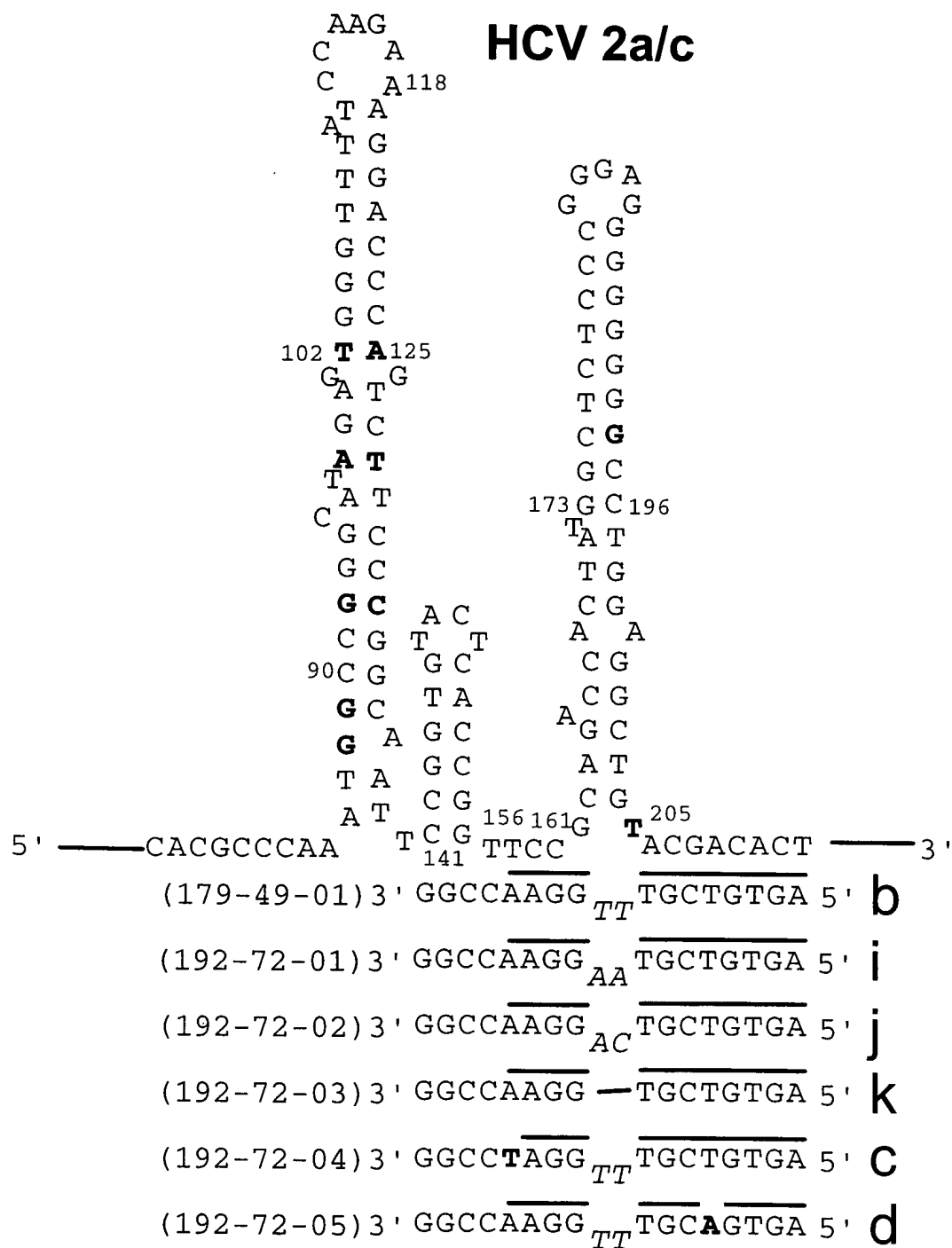


FIGURE 18D

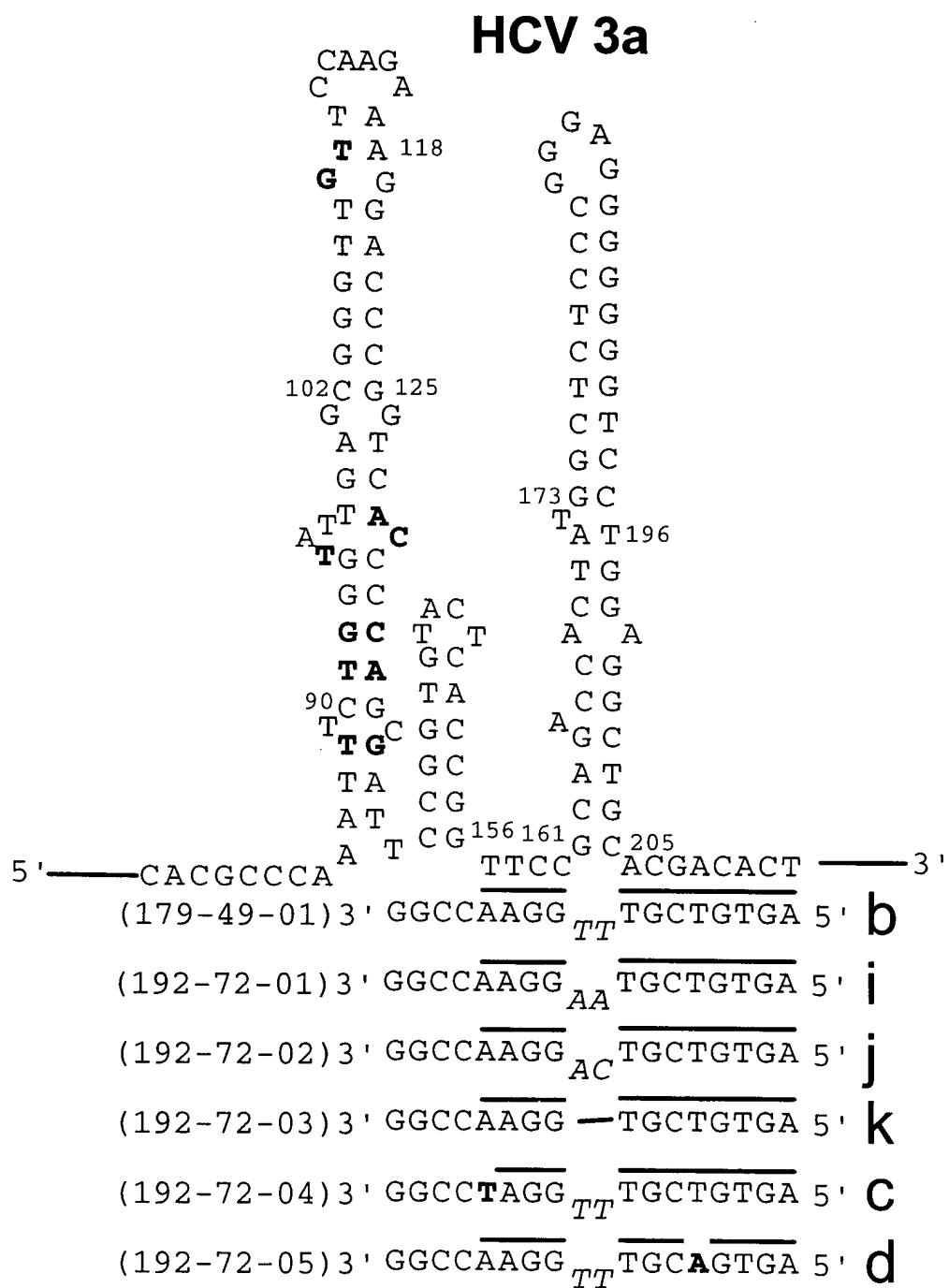


FIGURE 19

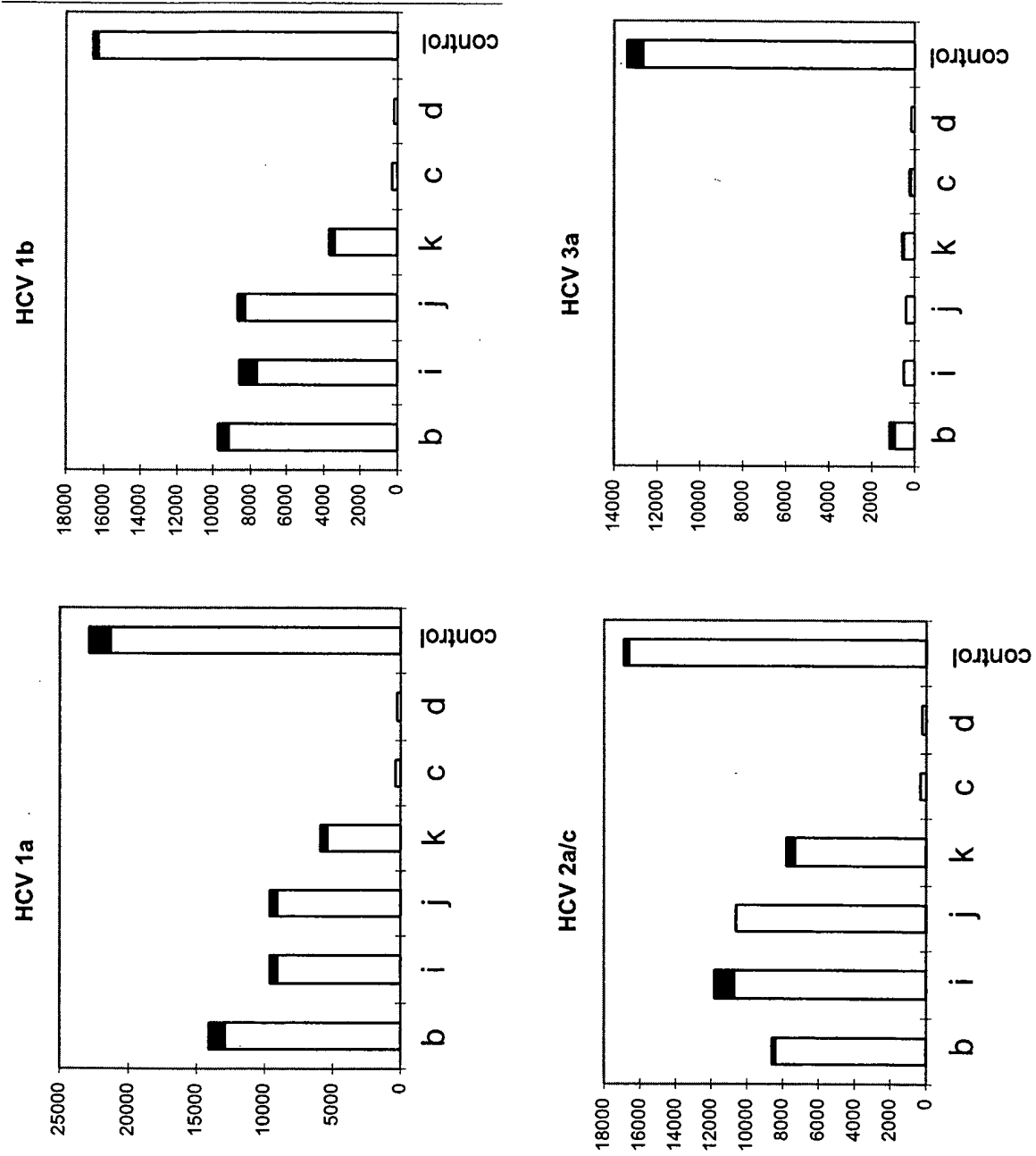
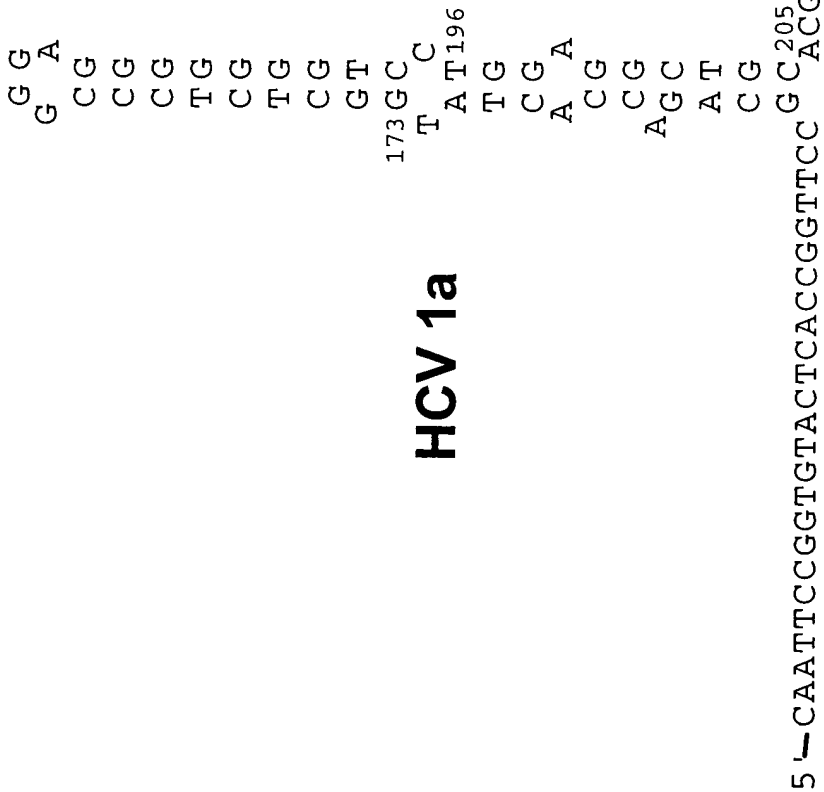


FIGURE 20A



- 3'-GGCCAAGGCTCTGGTGA-F1'5' (205-13-02)

a
- 3'-GGCCAAGG_{TT}TGCTGTGA-F1'5' (179-49-01)

b
- 3'-GGCC**T**AGG_{TT}TGCTGTGA-F1'5' (192-72-04)

c
- 3'-GGCCAAGG_{TT}TGC**A**GTGA-F1'5' (192-72-05)

d
- 3'-GGCCAAGG-F15' (205-27-01)

e

FIGURE 20B

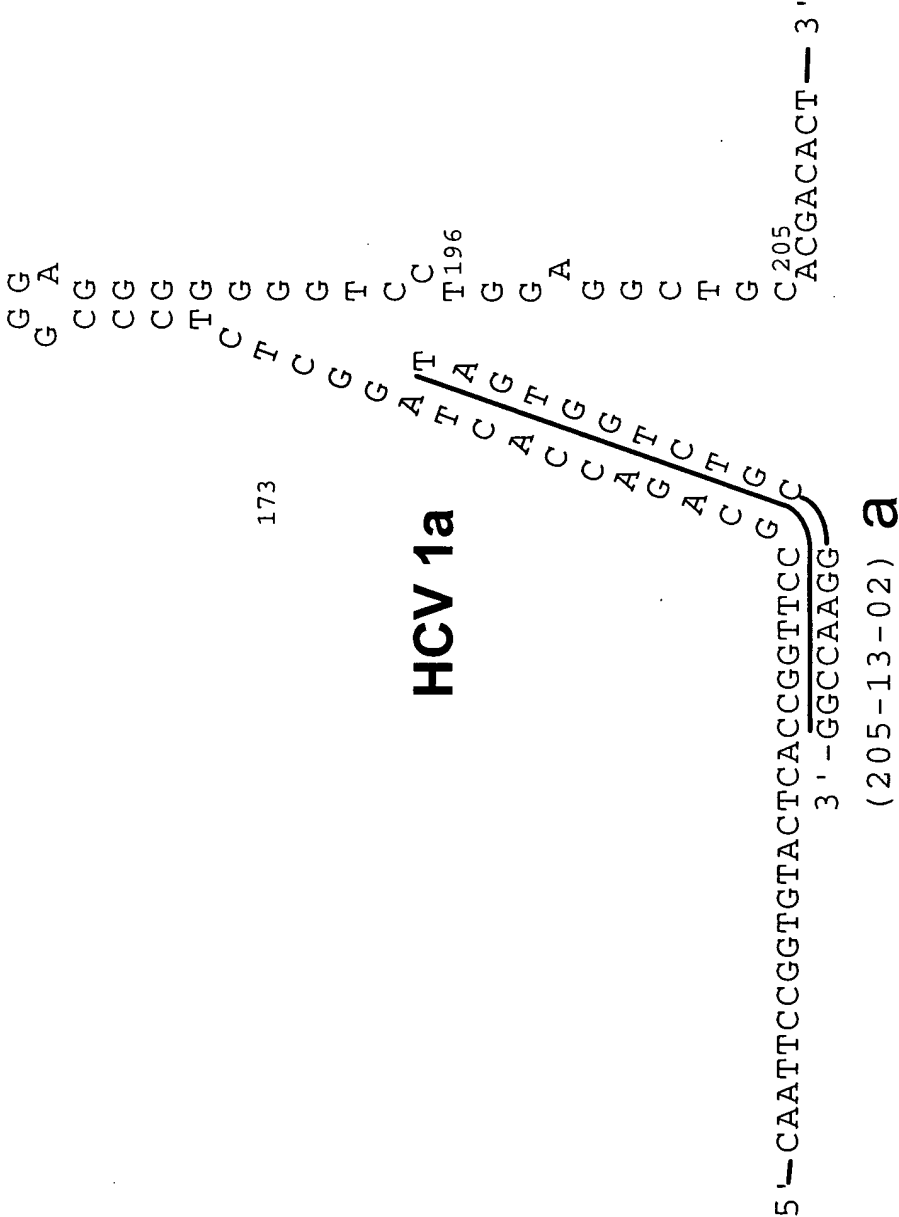


FIGURE 22

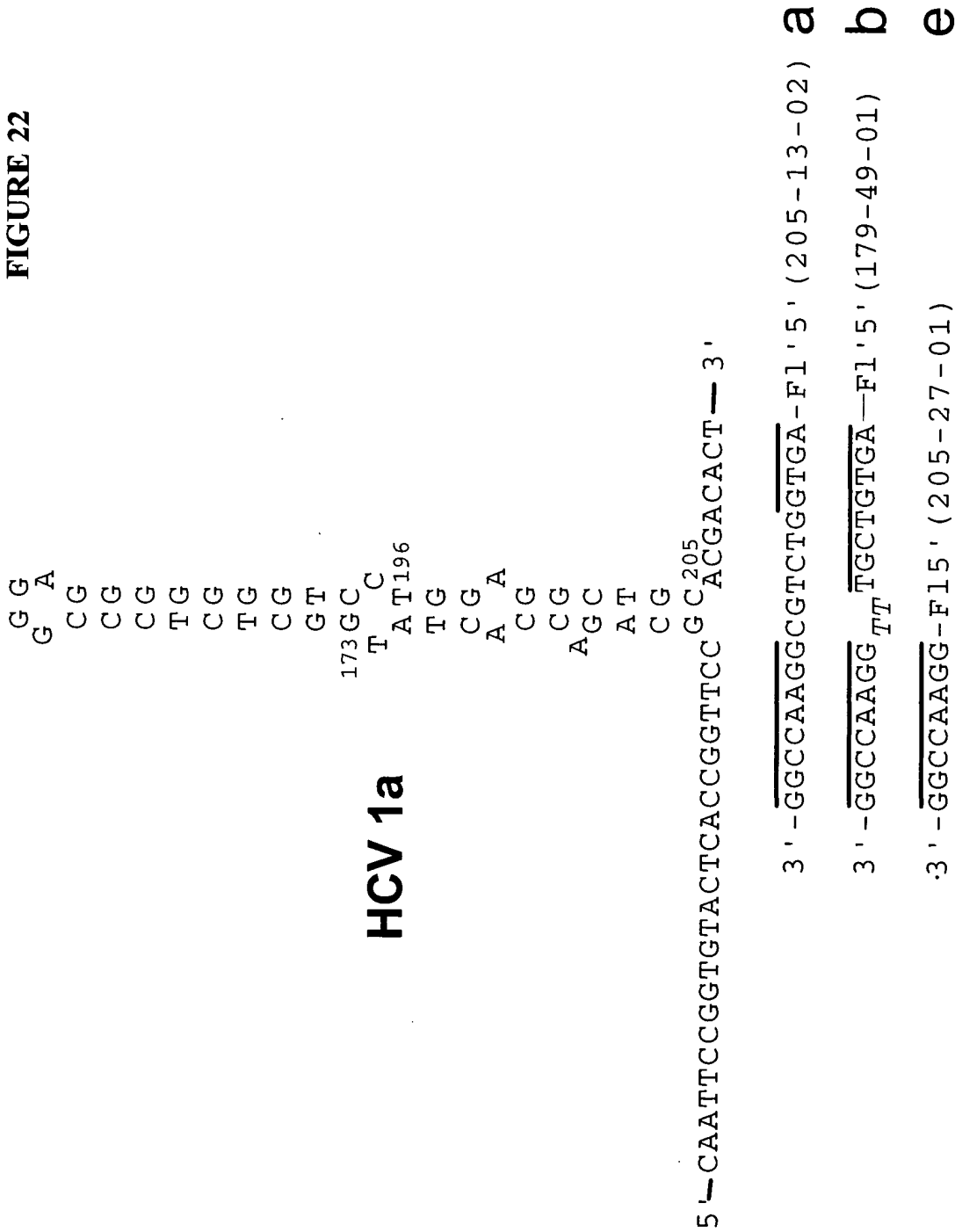


FIGURE 23

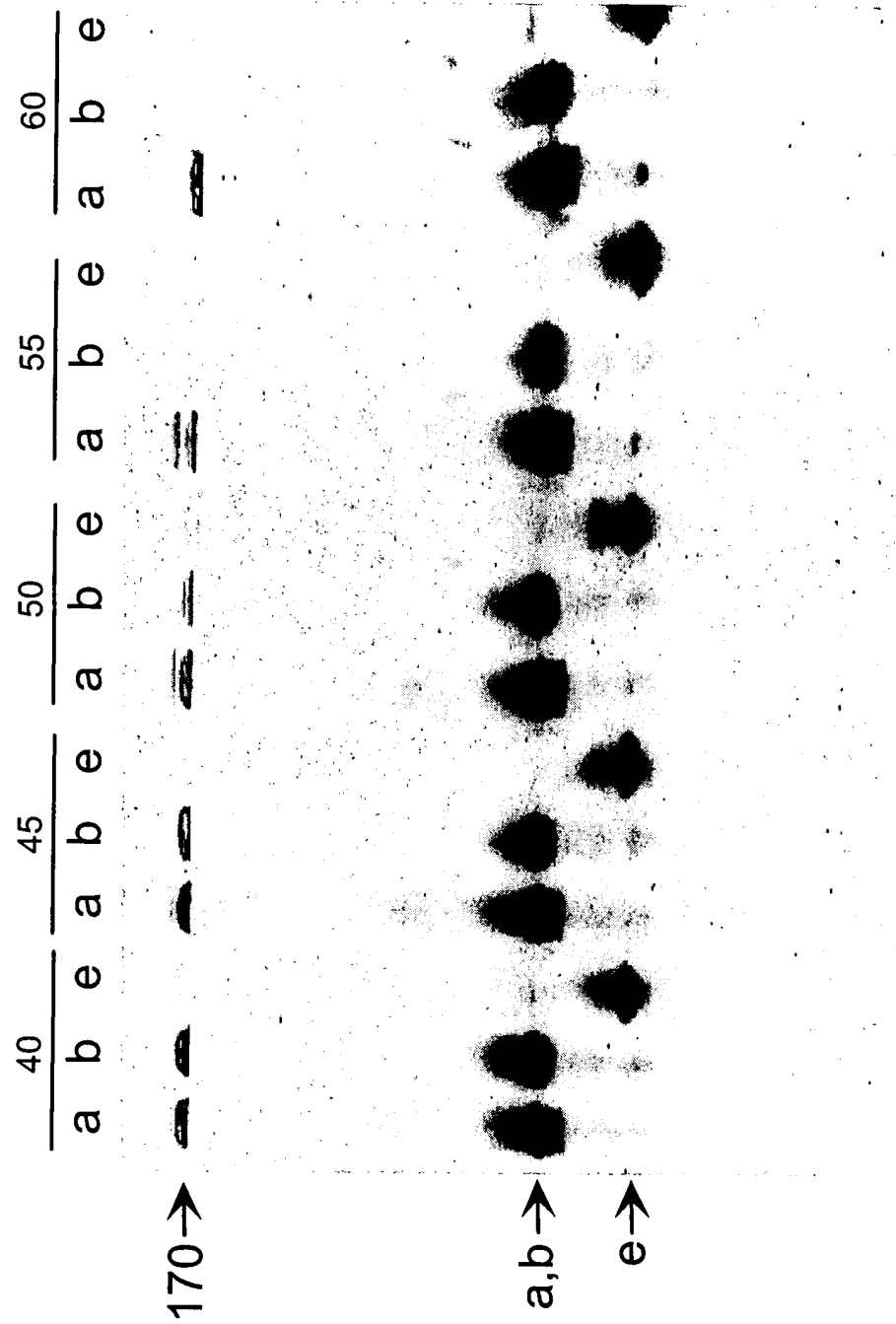


FIGURE 24

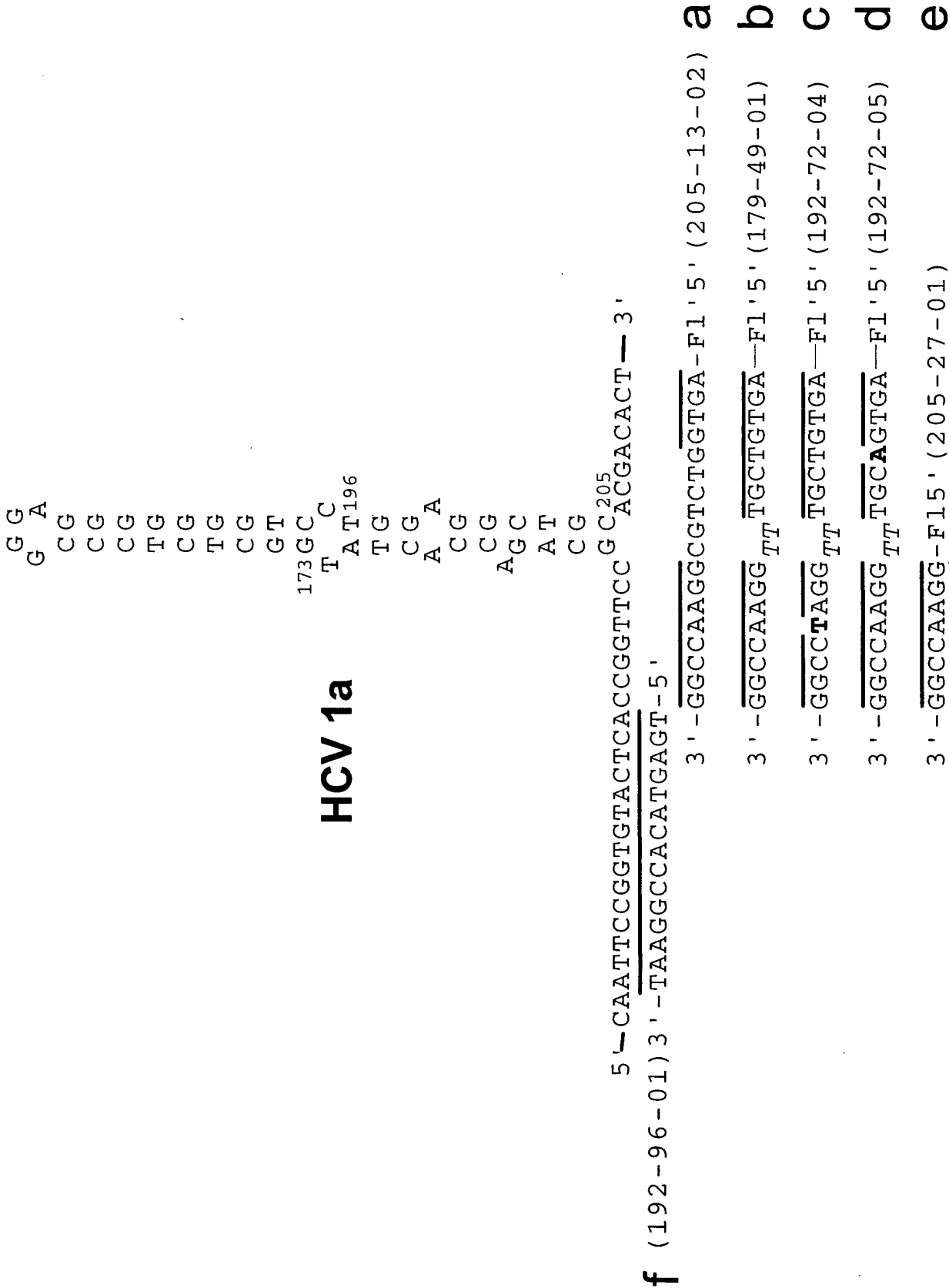


FIGURE 25

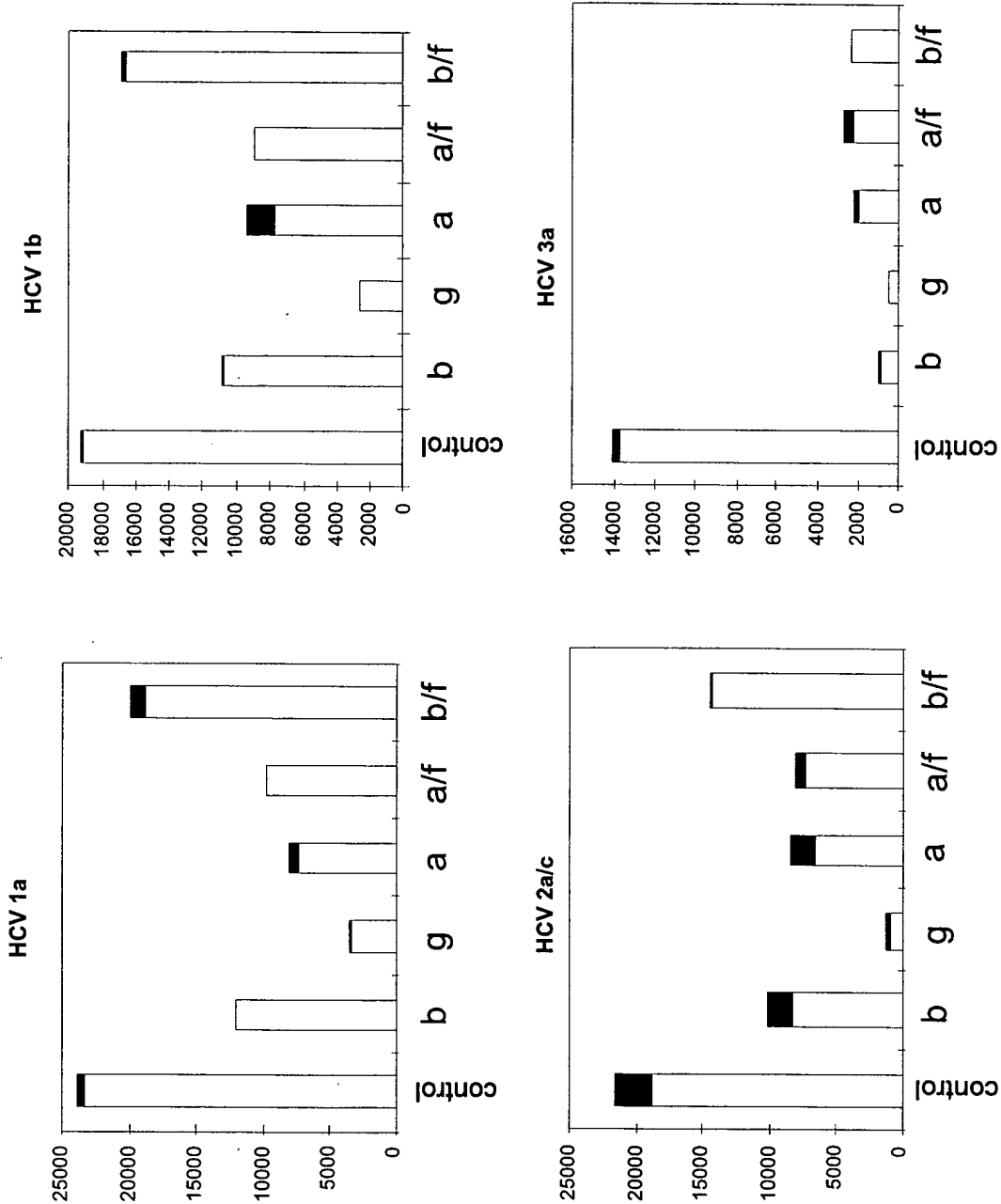


FIGURE 26

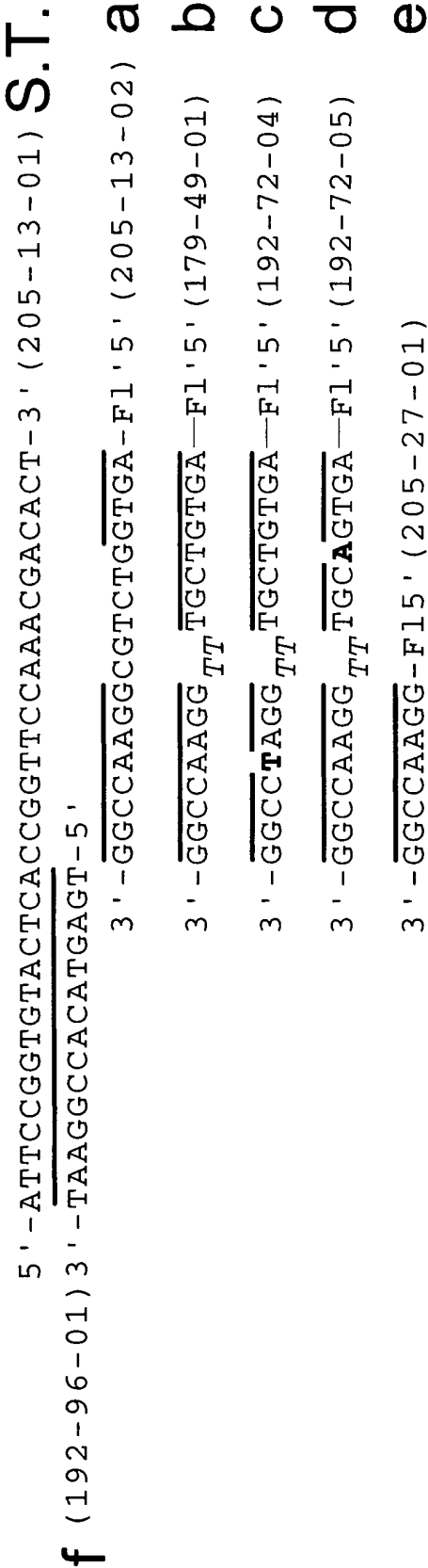


FIGURE 27

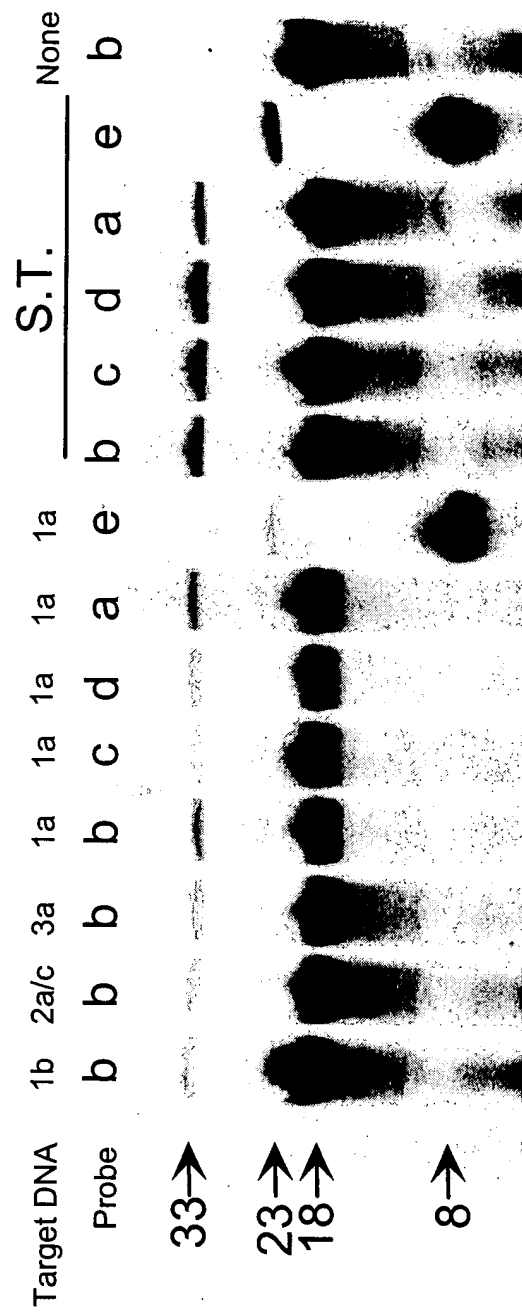
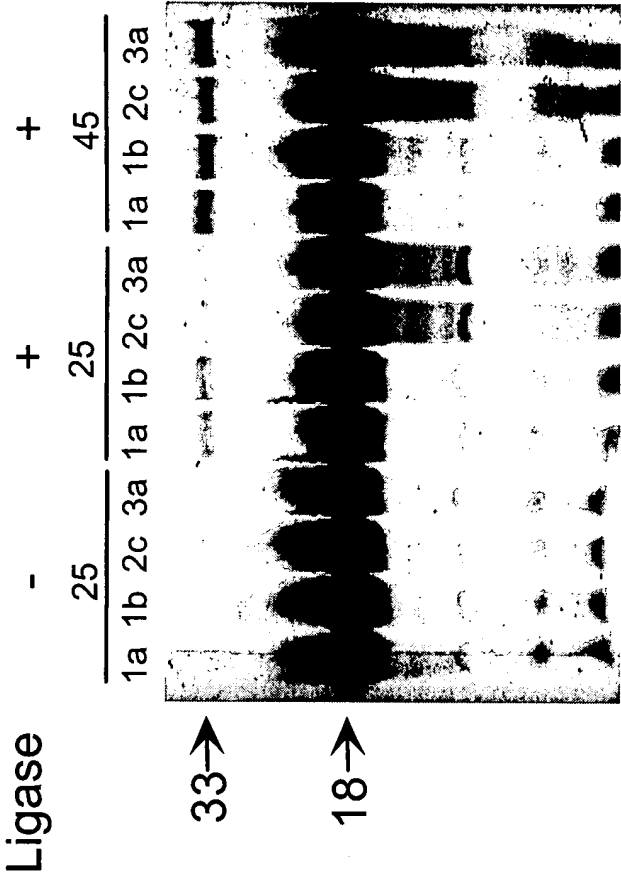


FIGURE 28



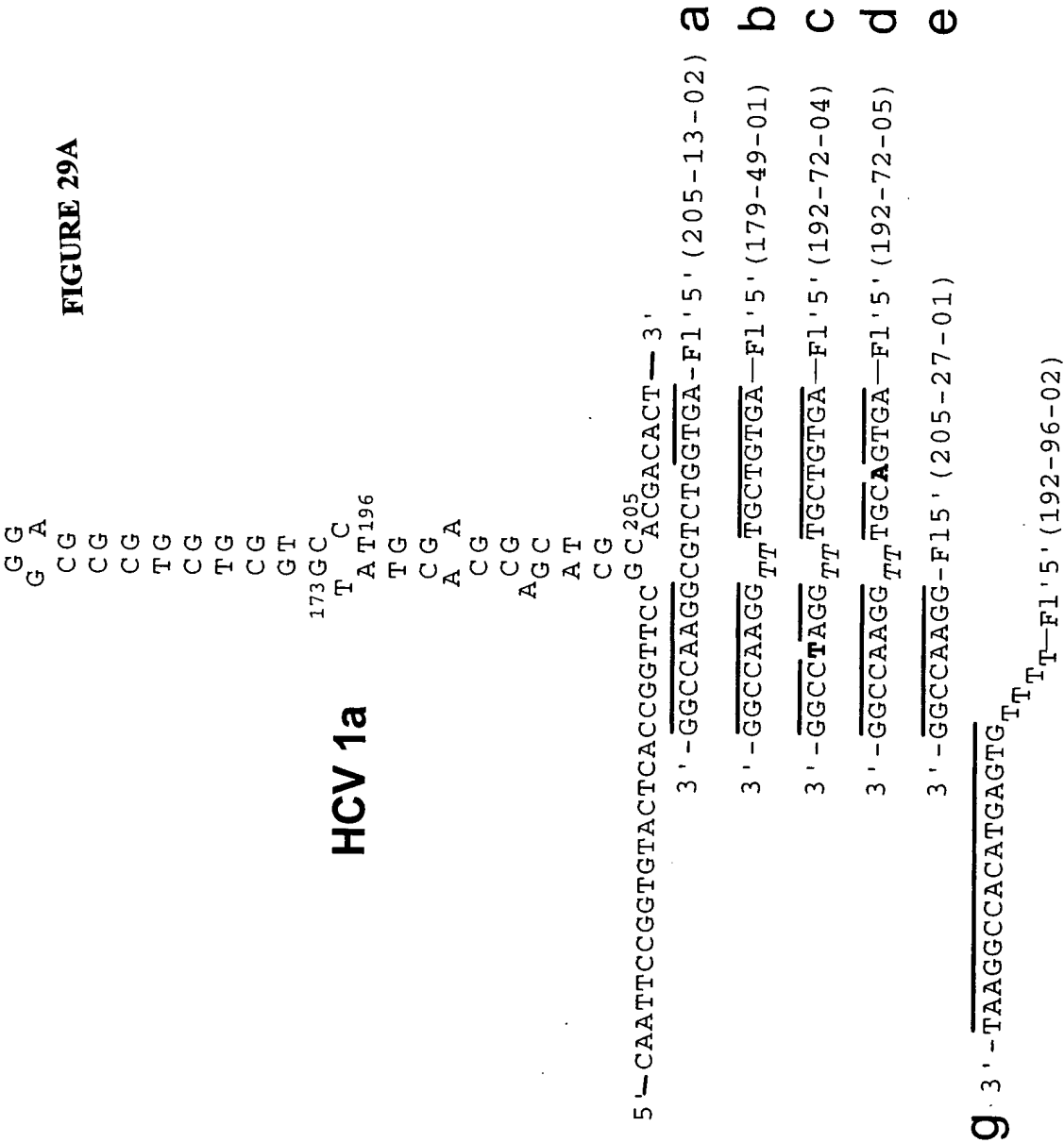


FIGURE 29B

5' -ATCCGGTGTA CTACCGGTTCCAAACGACACT-3' (205-13-01) **S.T.**

3' -GGCCAAAGCGTCTGGTGA-F1'5' (205-13-02) **a**

3' -GGCCAAAGG_{TT}TGCTGTGA-F1'5' (179-49-01) **b**

3' -GGCC**T**AGG_{TT}TGCTGTGA-F1'5' (192-72-04) **c**

3' -GGCCAAAGG_{TT}TGC**A**GTGA-F1'5' (192-72-05) **d**

3' -GGCCAAAGG-F15' (205-27-01) **e**

g 3' -TAAGGCCACATGAGTG_{TT}_{TT}-F1'5' (192-96-02)

FIGURE 30



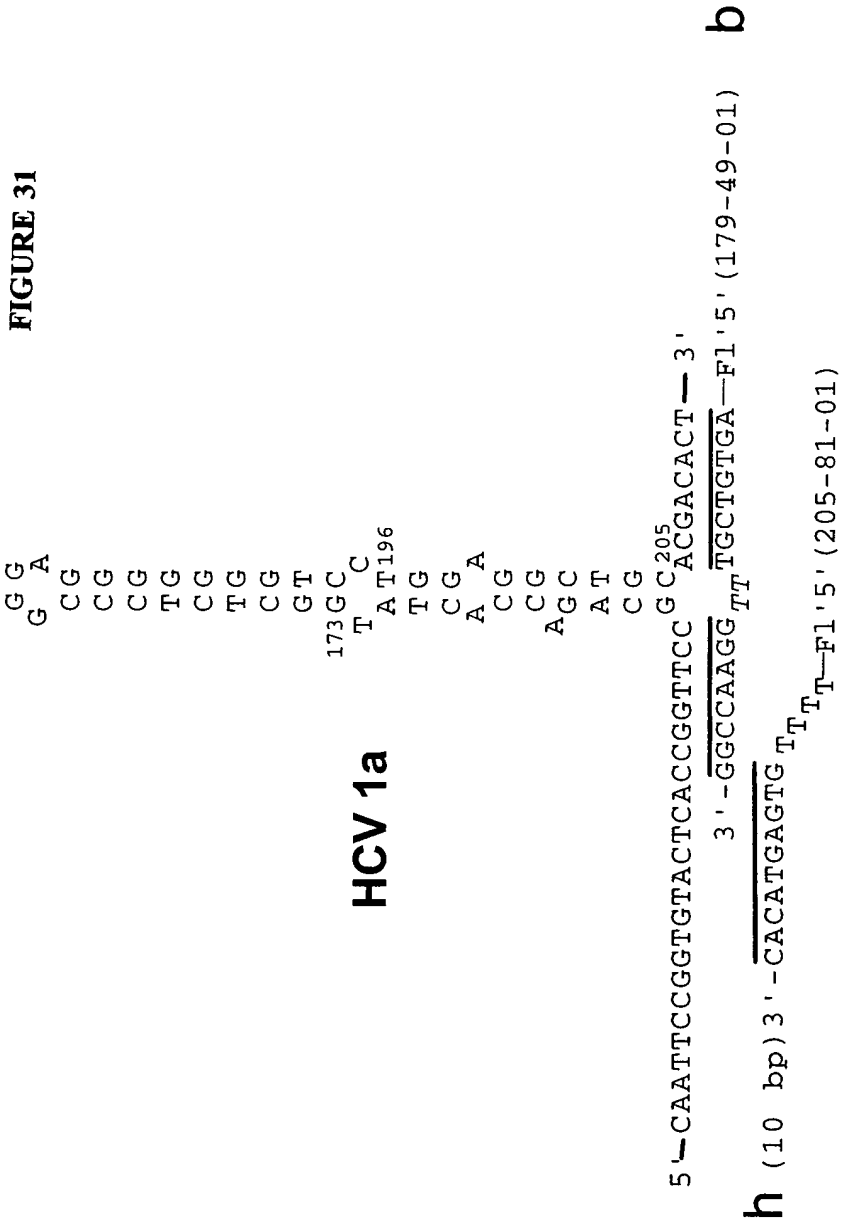


FIGURE 32

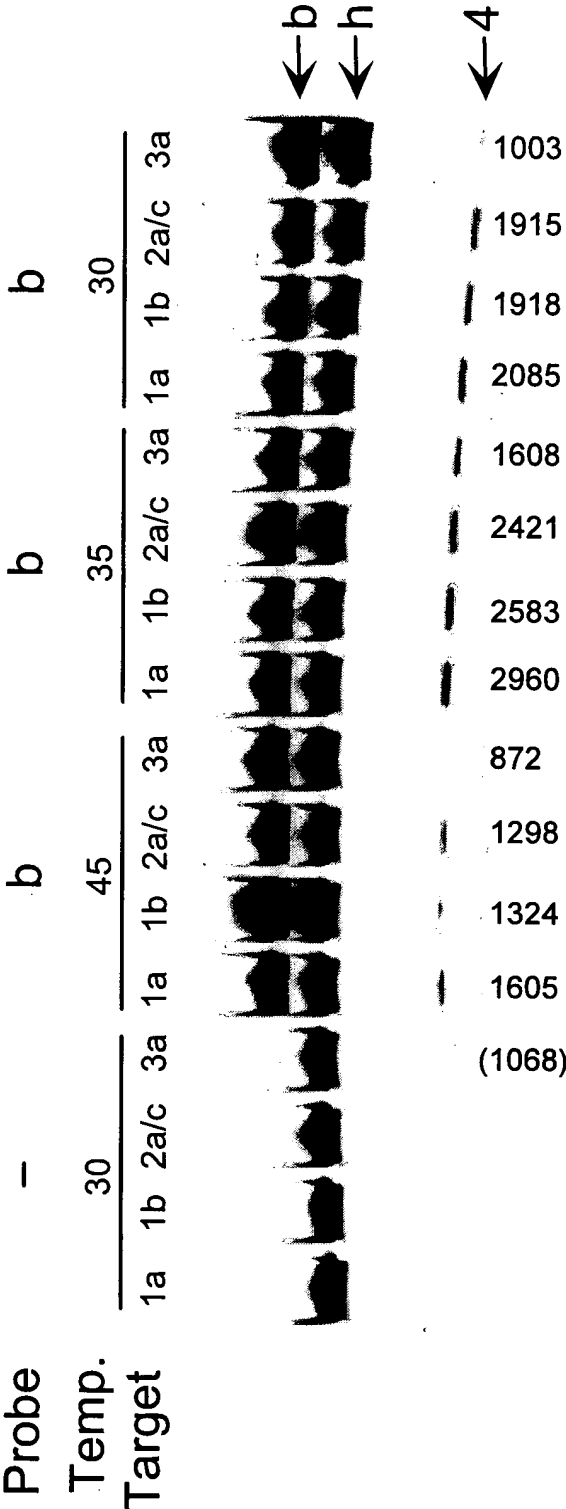


FIGURE 34

STEPS

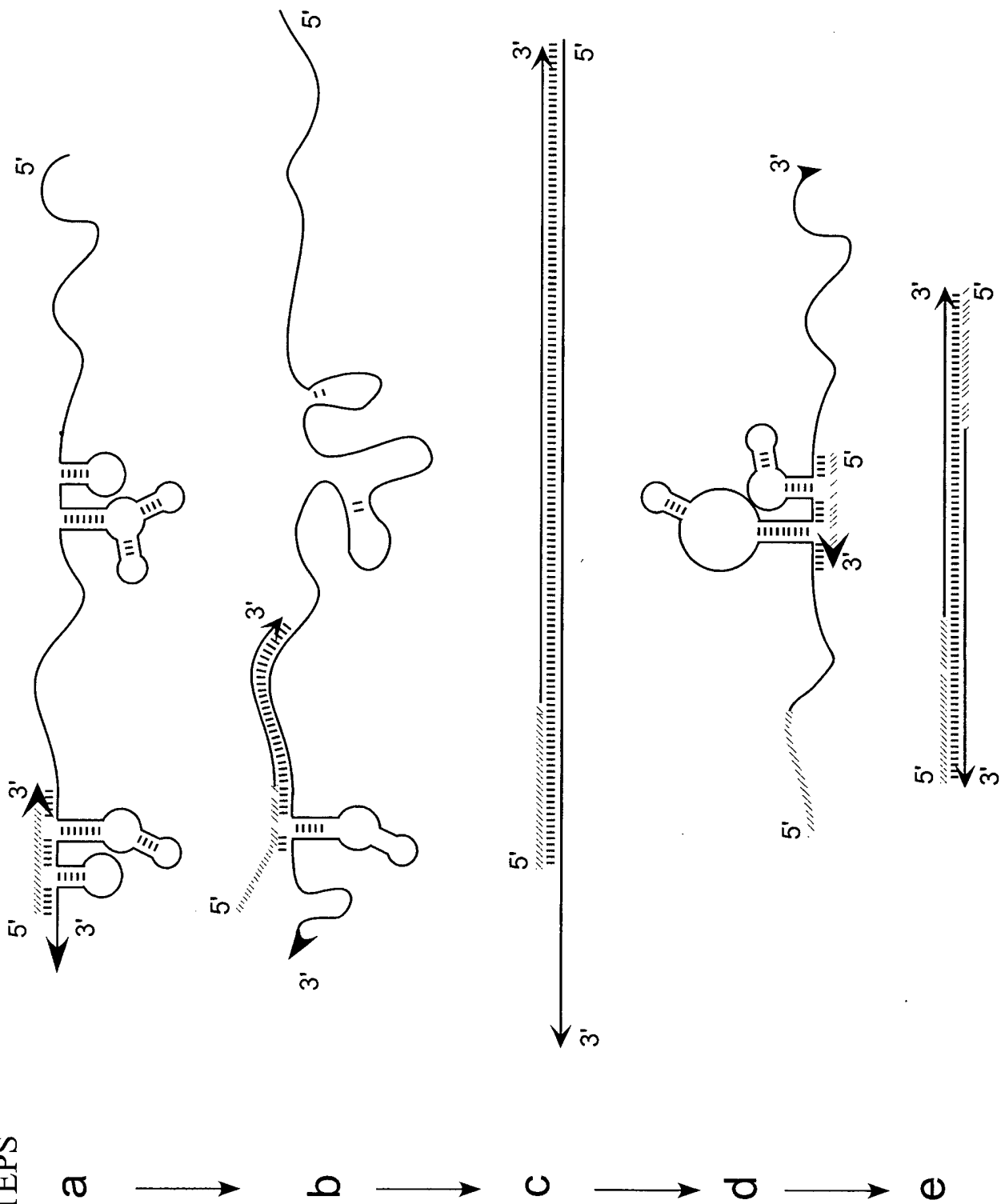


FIGURE 36

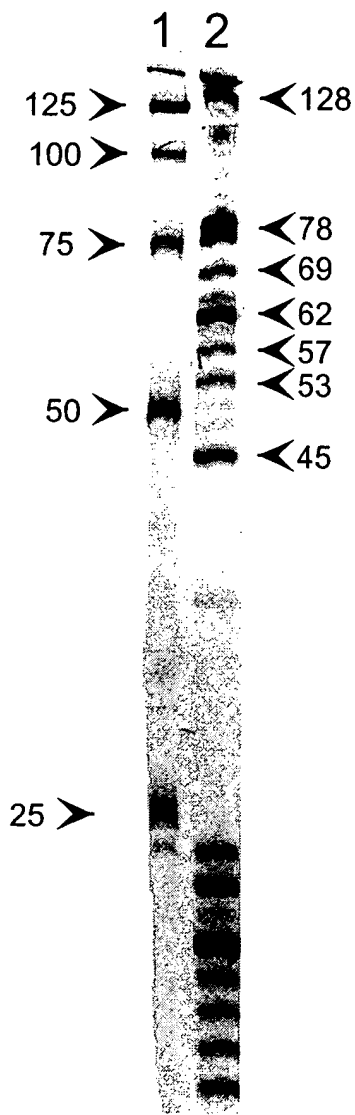


FIGURE 37A

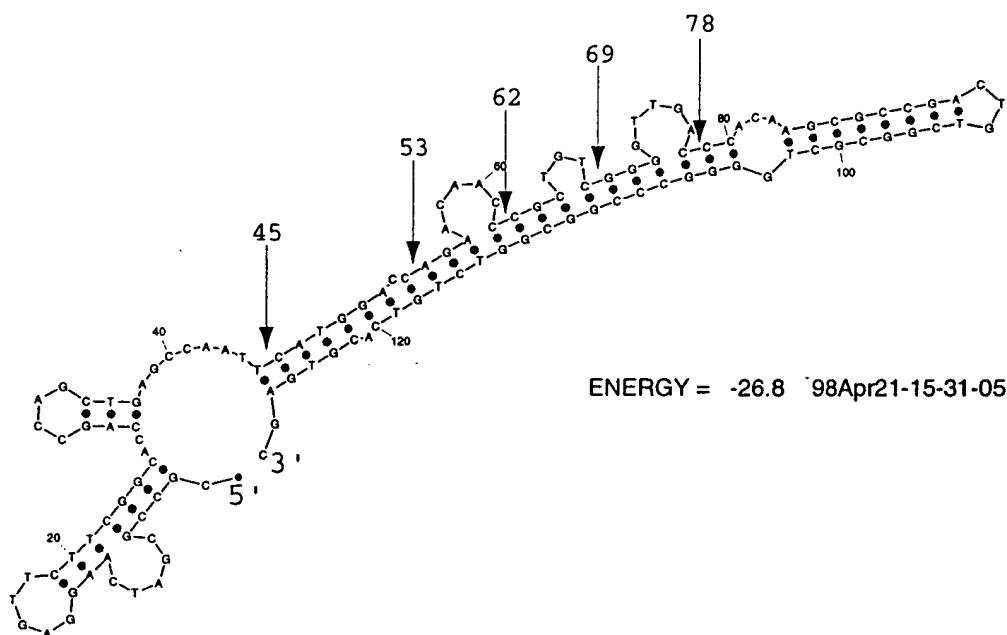
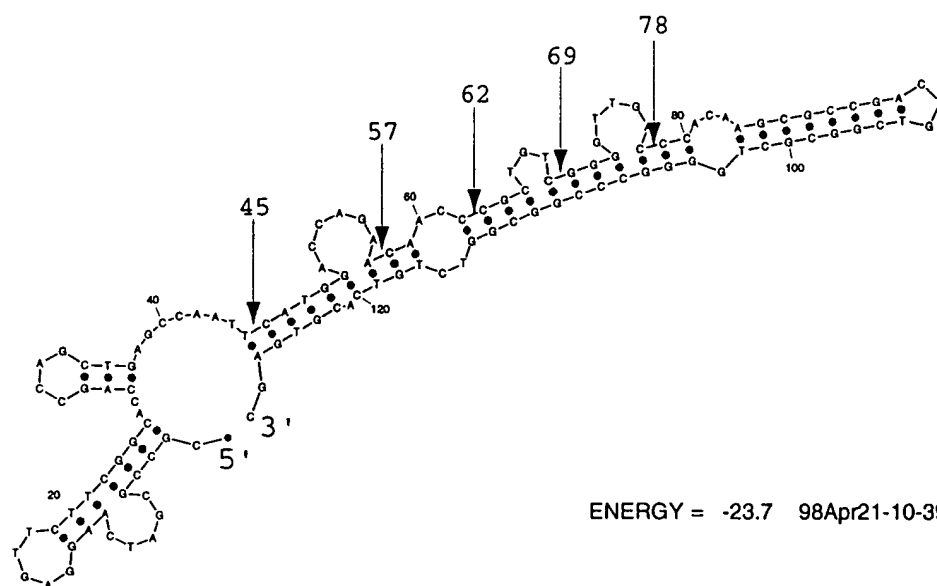


FIGURE 37B

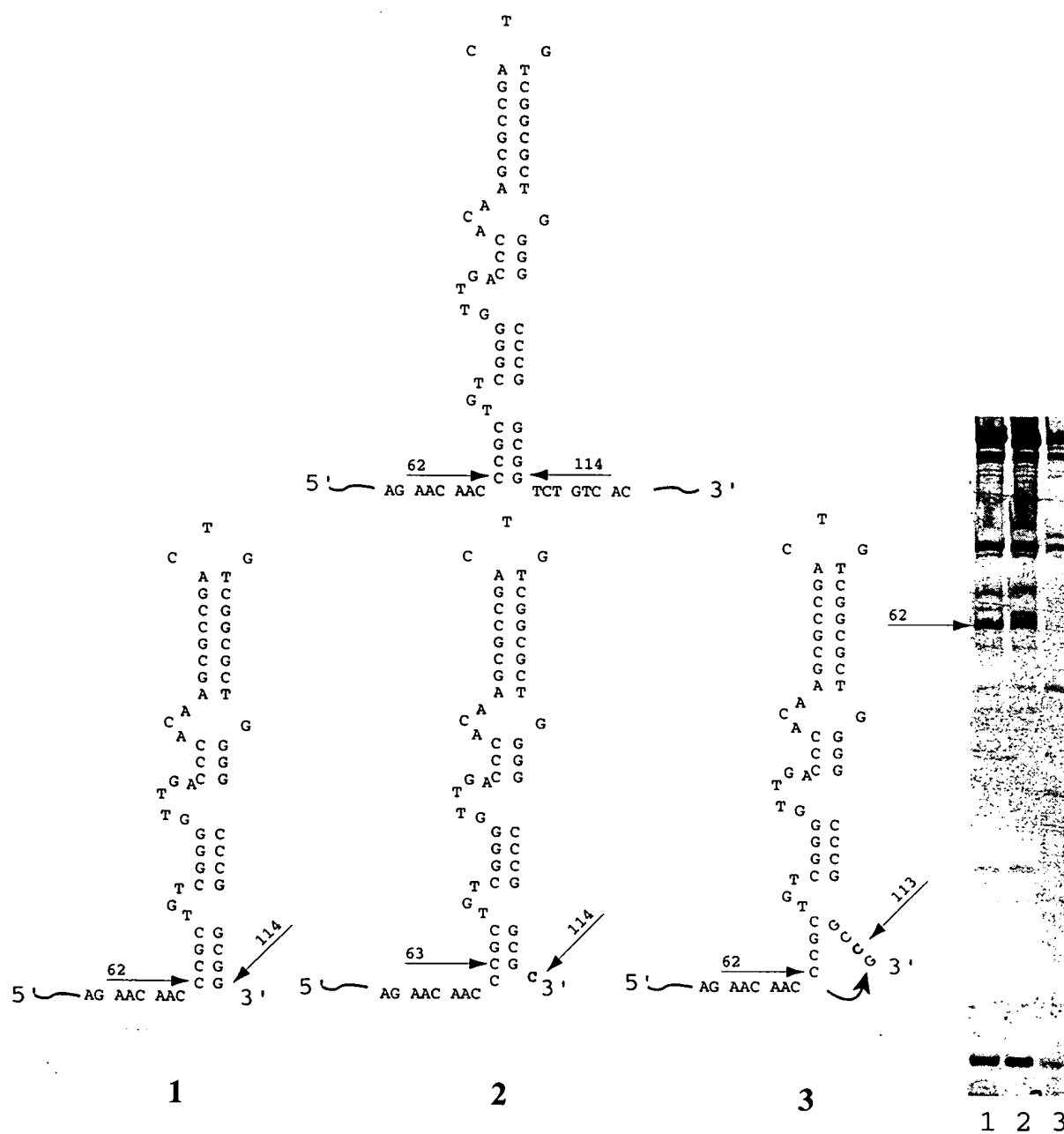


FIGURE 37C

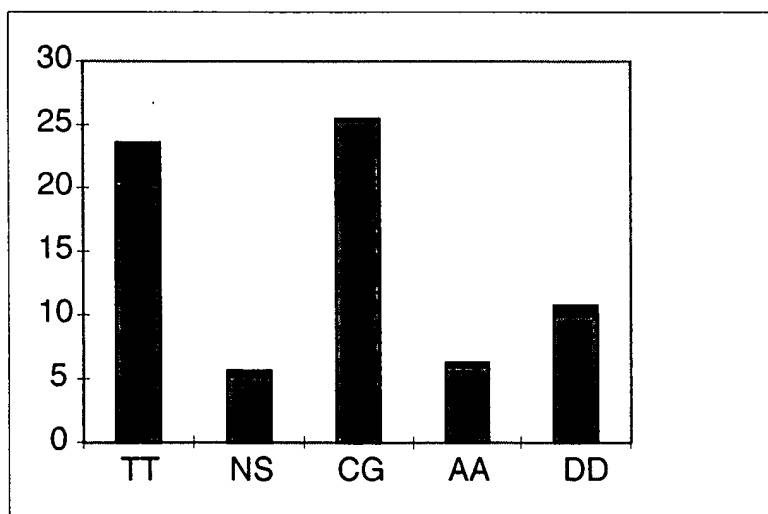
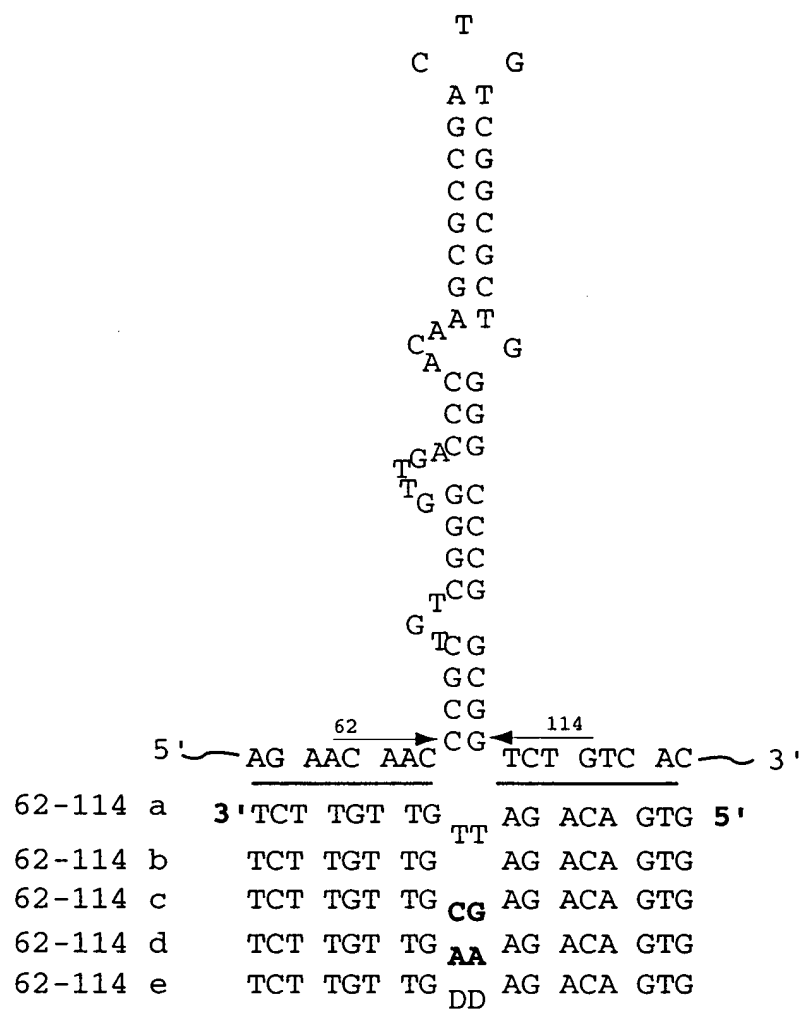


FIGURE 38A

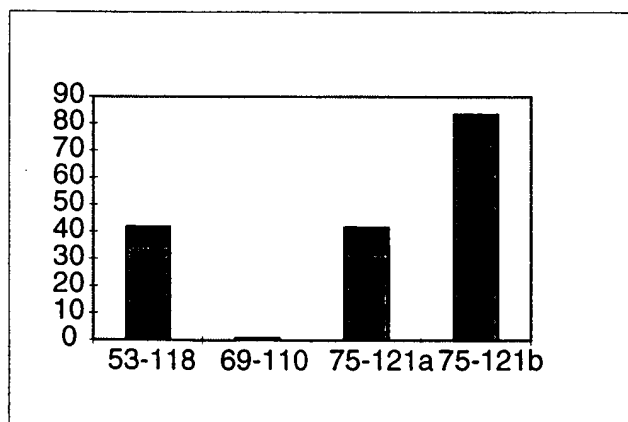
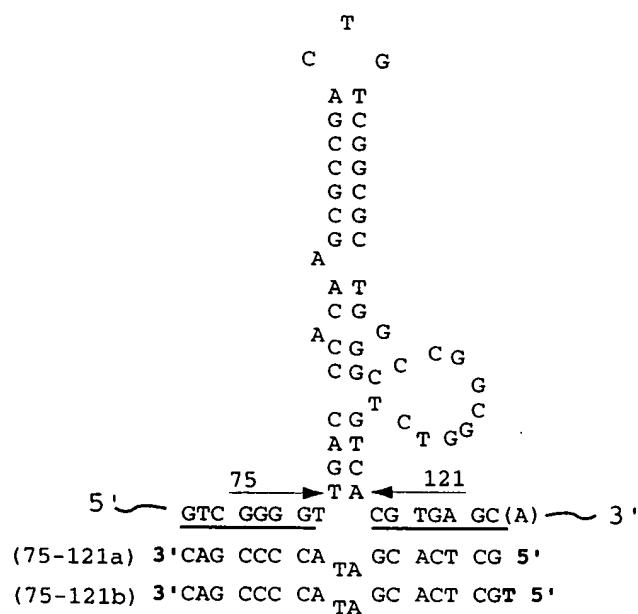
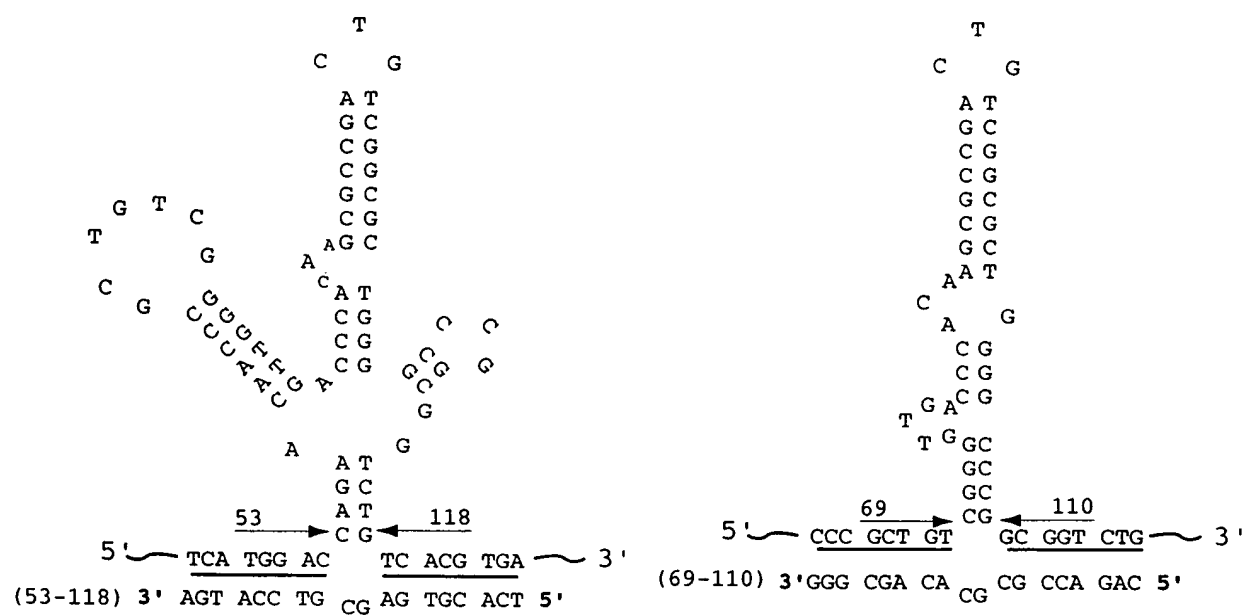


FIGURE 38B

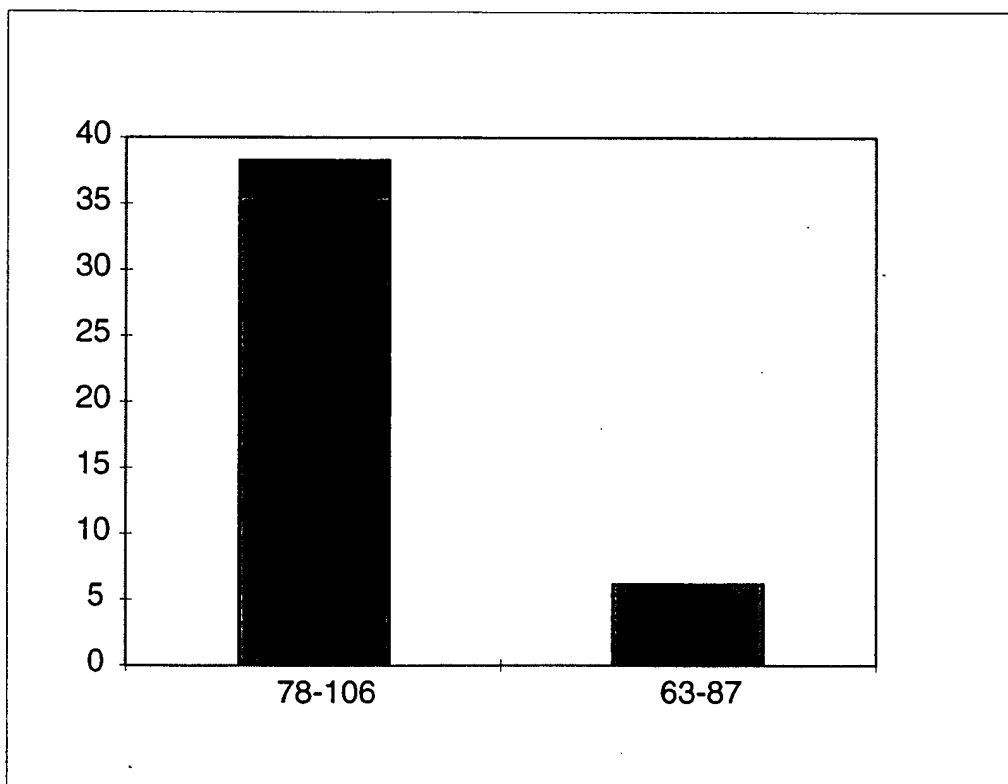
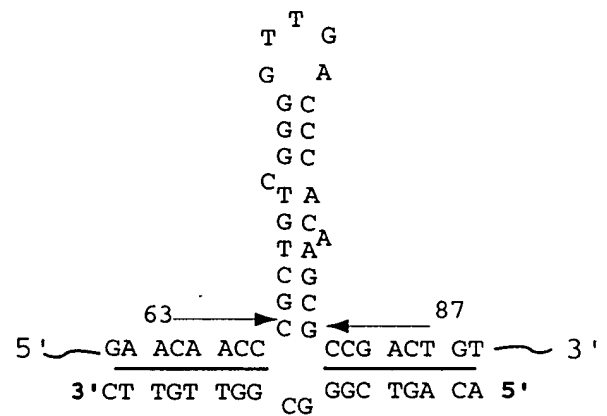
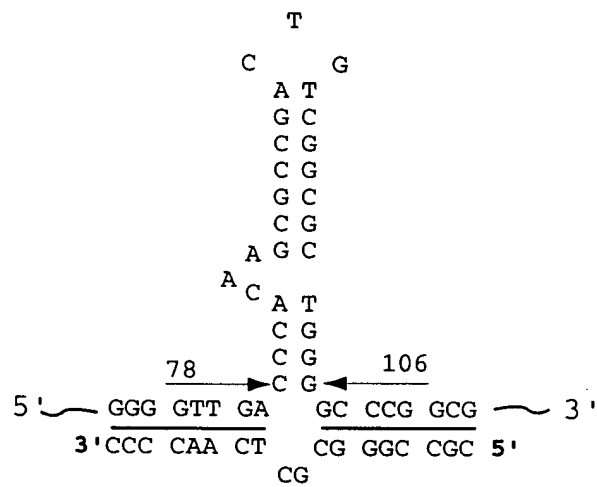


FIGURE 38C

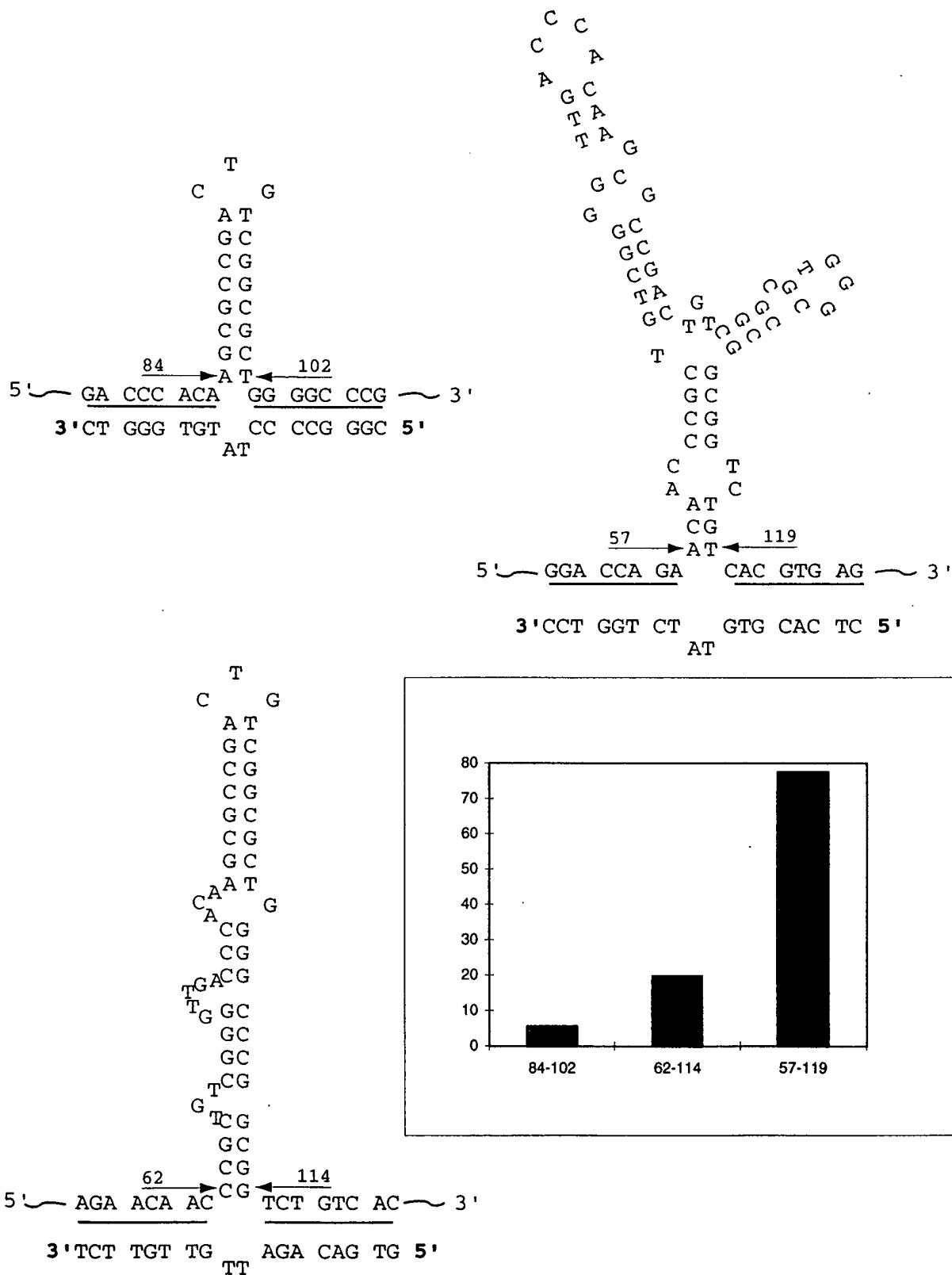


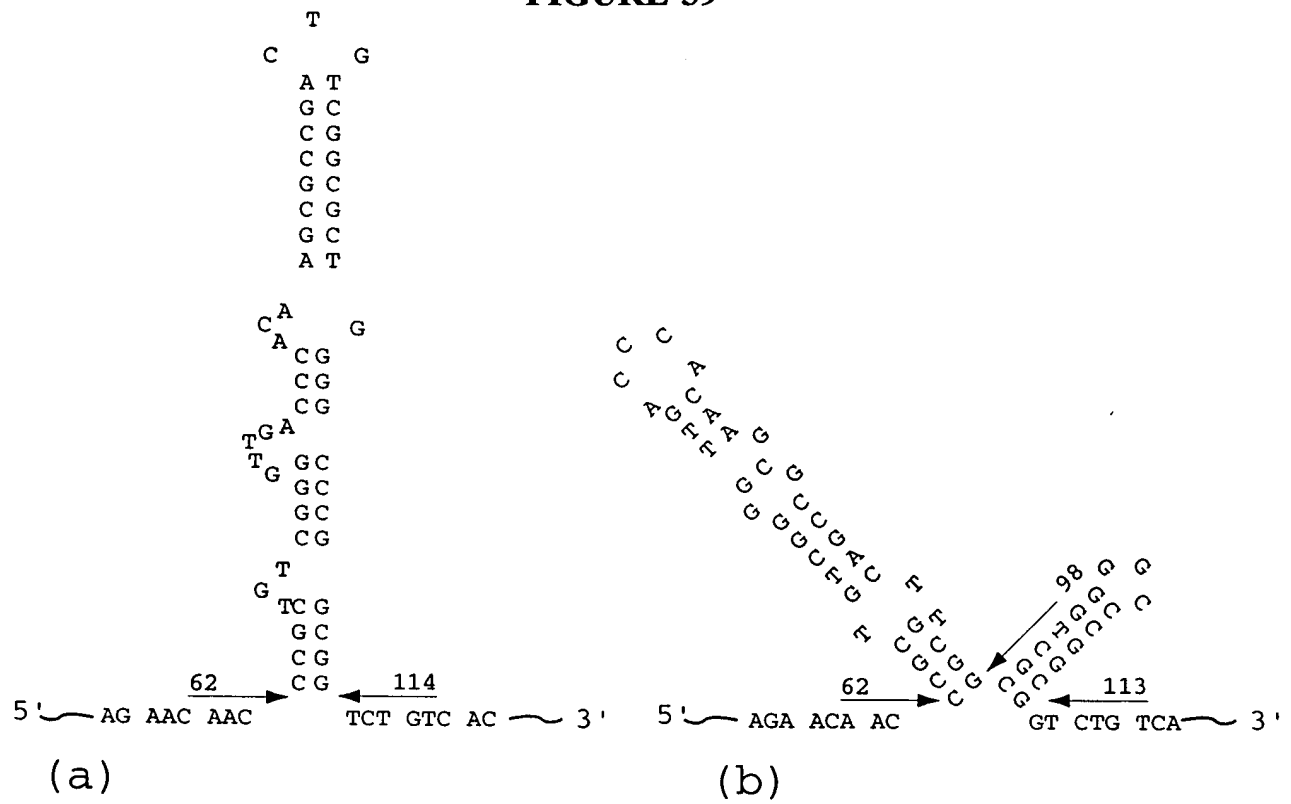
FIGURE 39

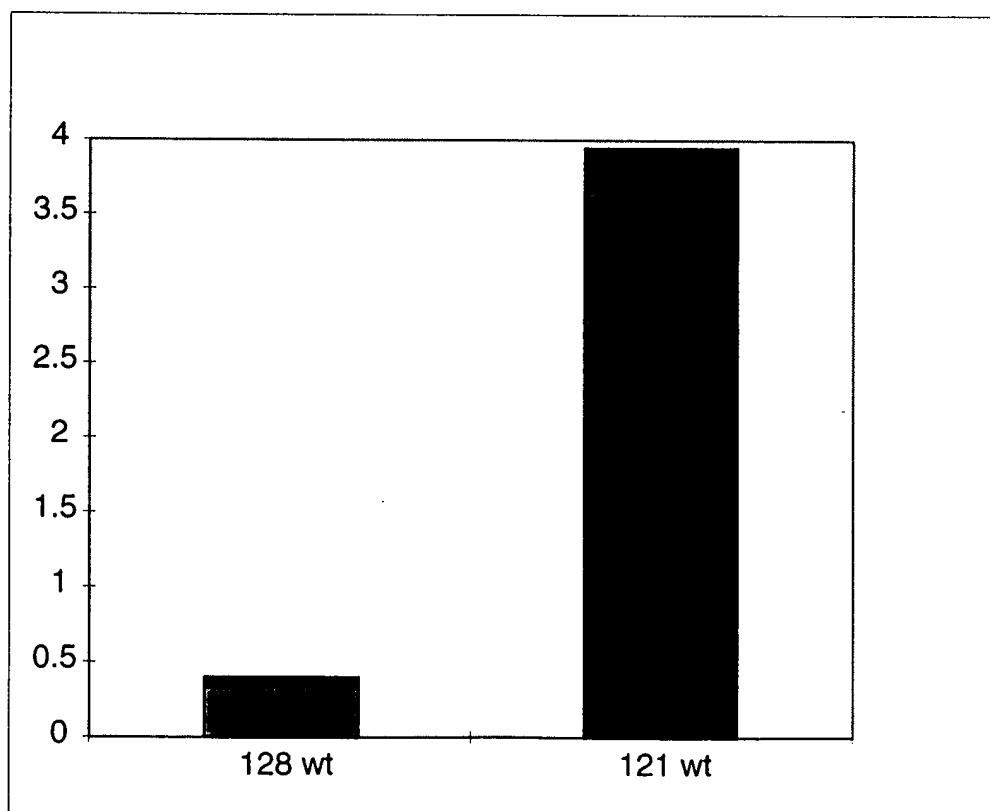
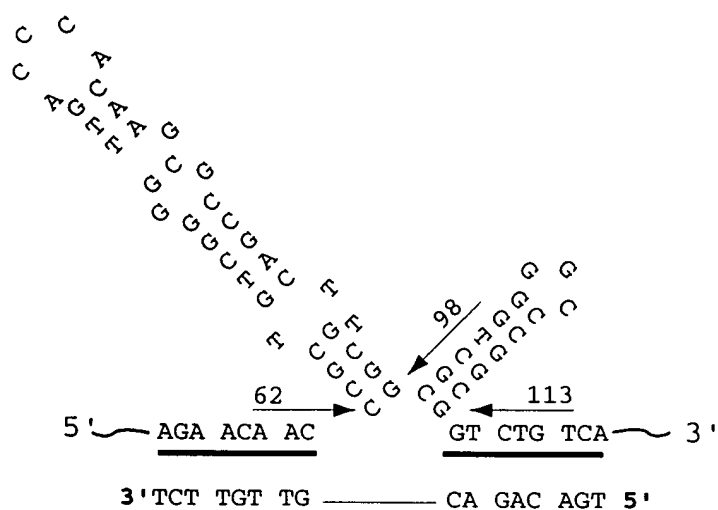
FIGURE 40

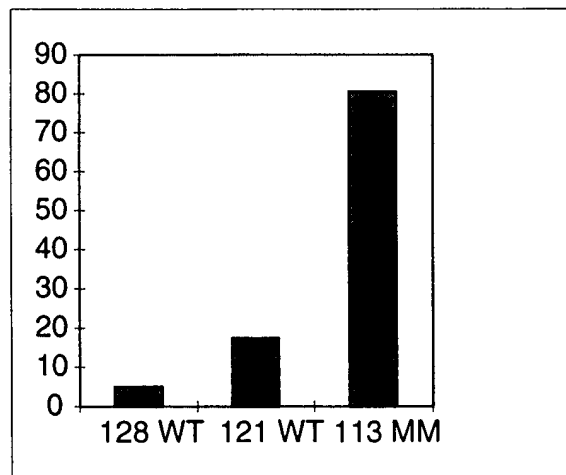
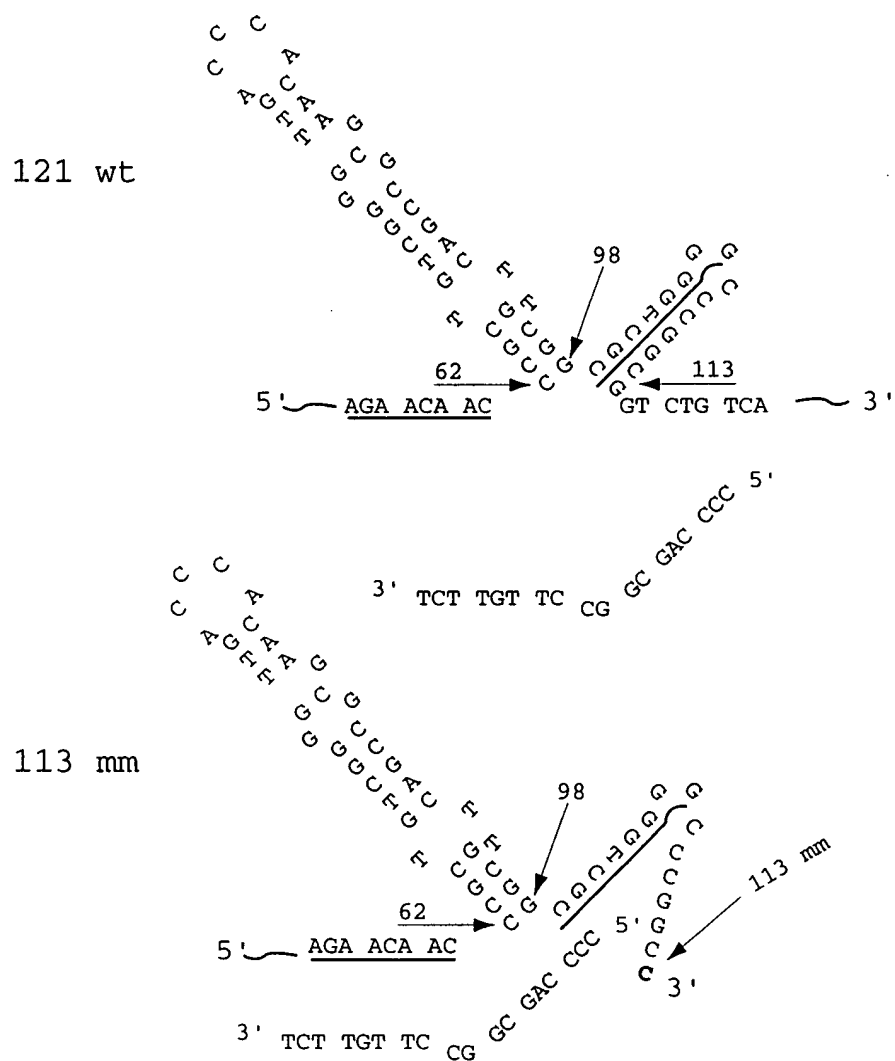
FIGURE 41

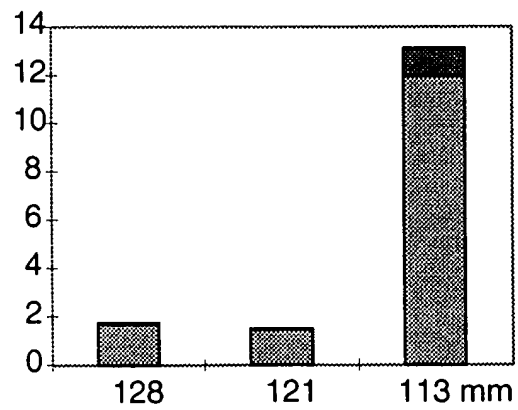
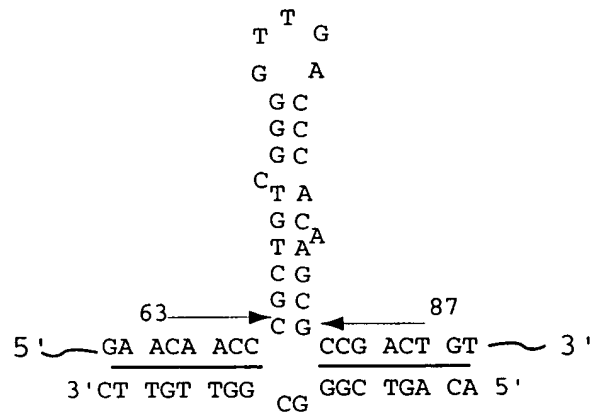
FIGURE 42

FIGURE 43A

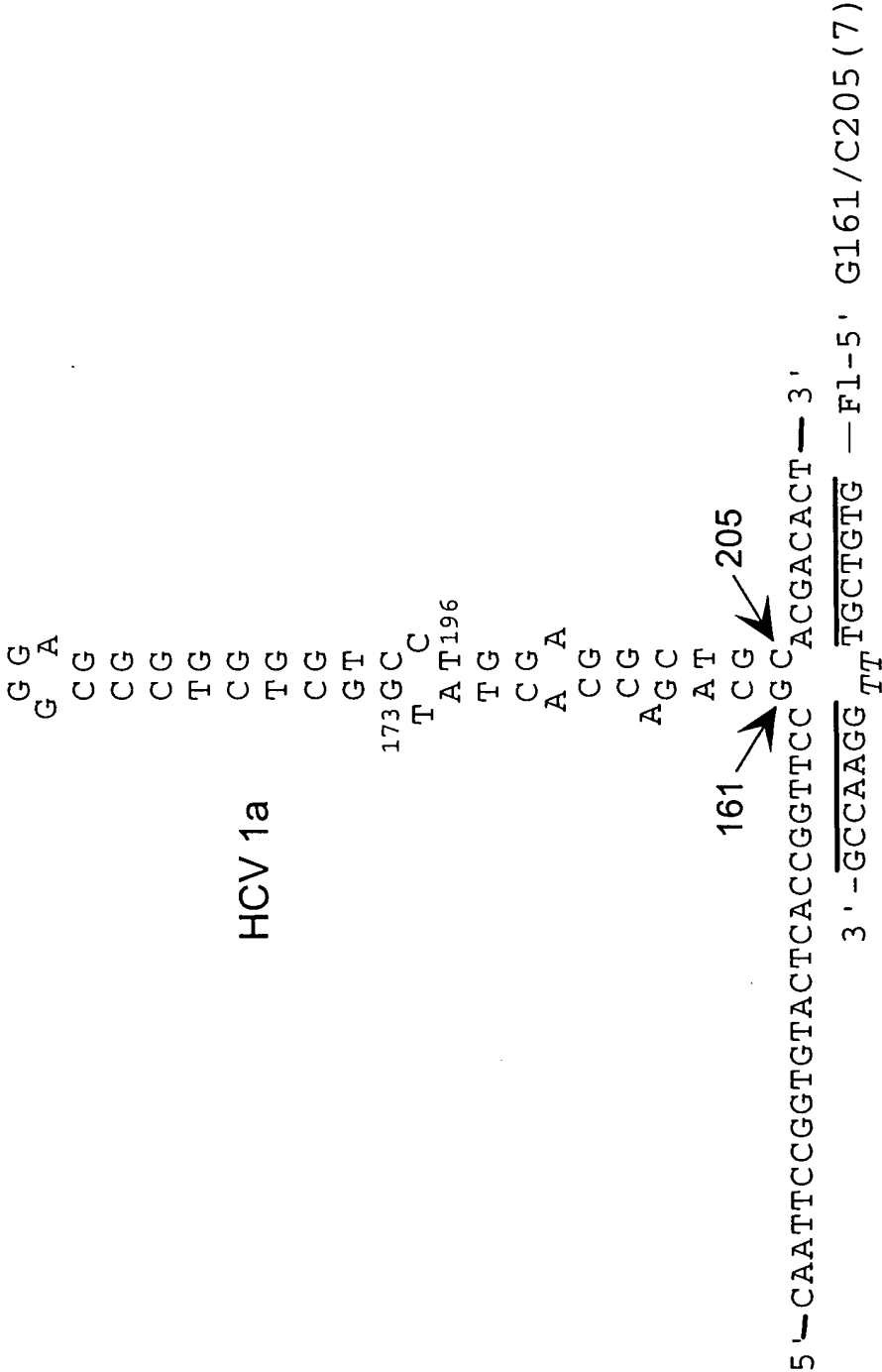


FIGURE 43B

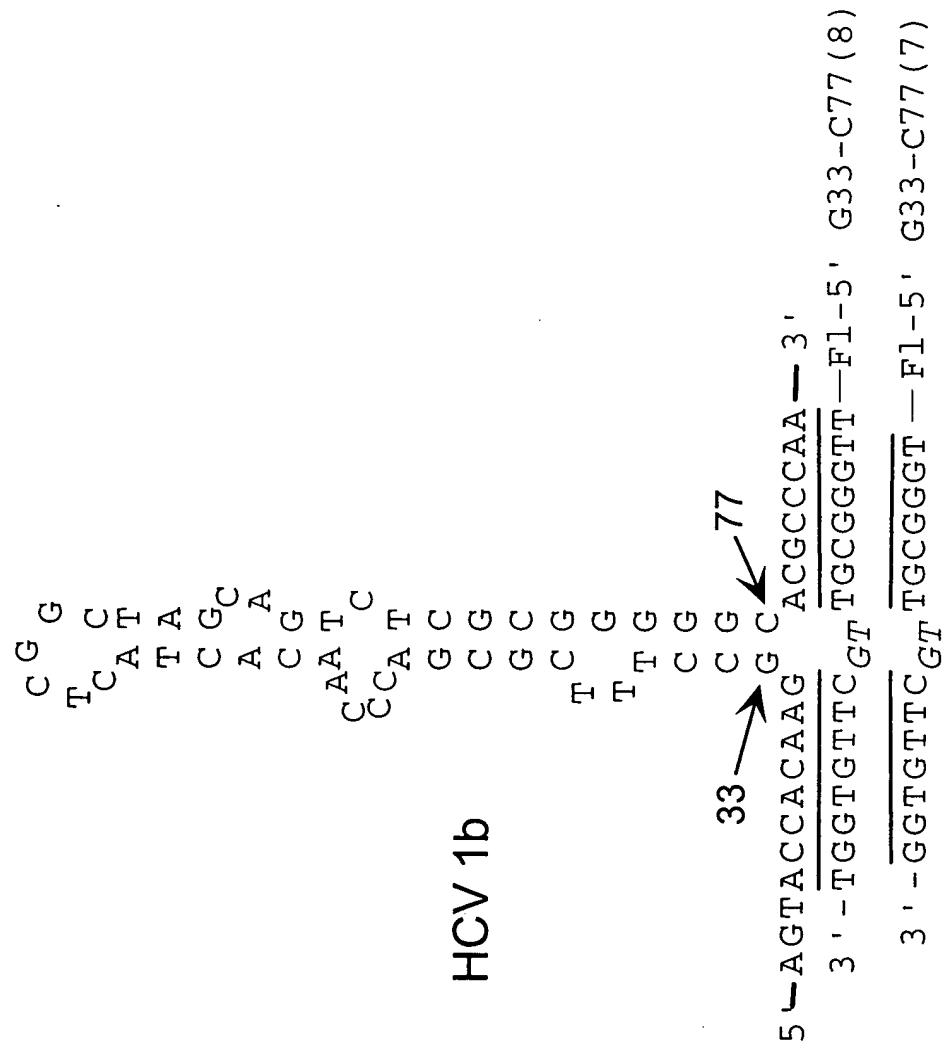


FIGURE 44A

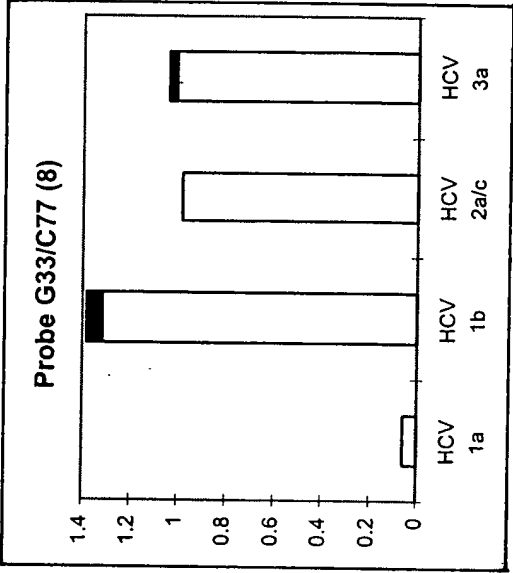
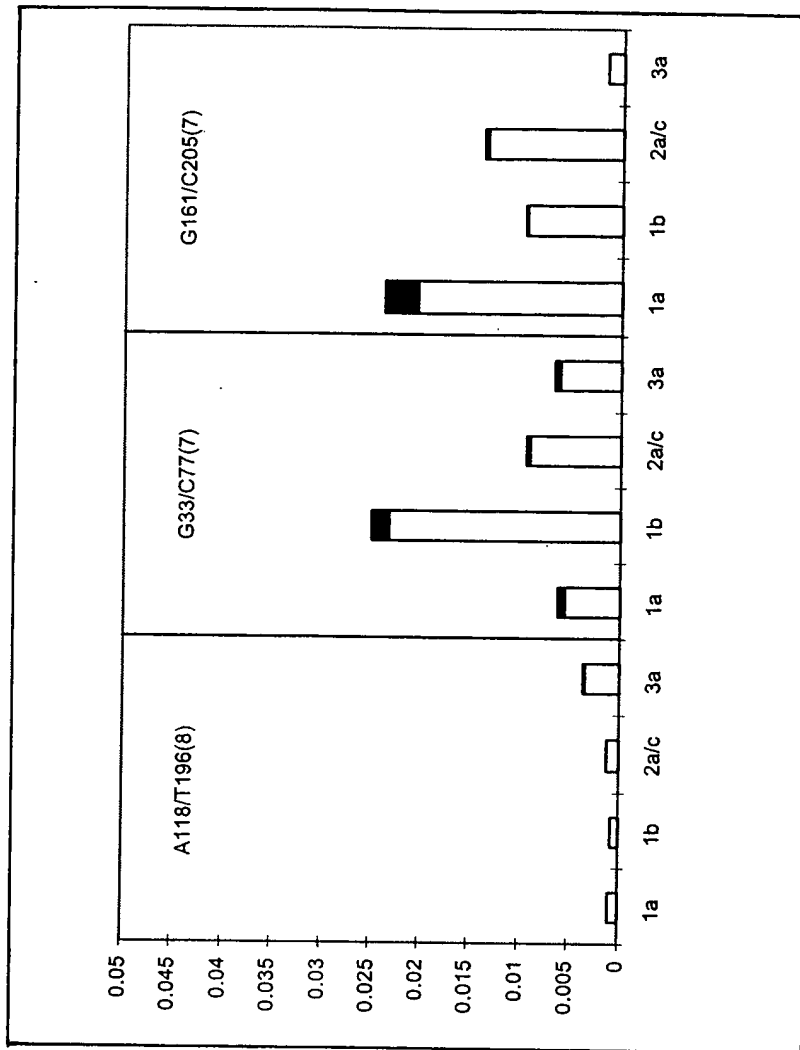


FIGURE 44B



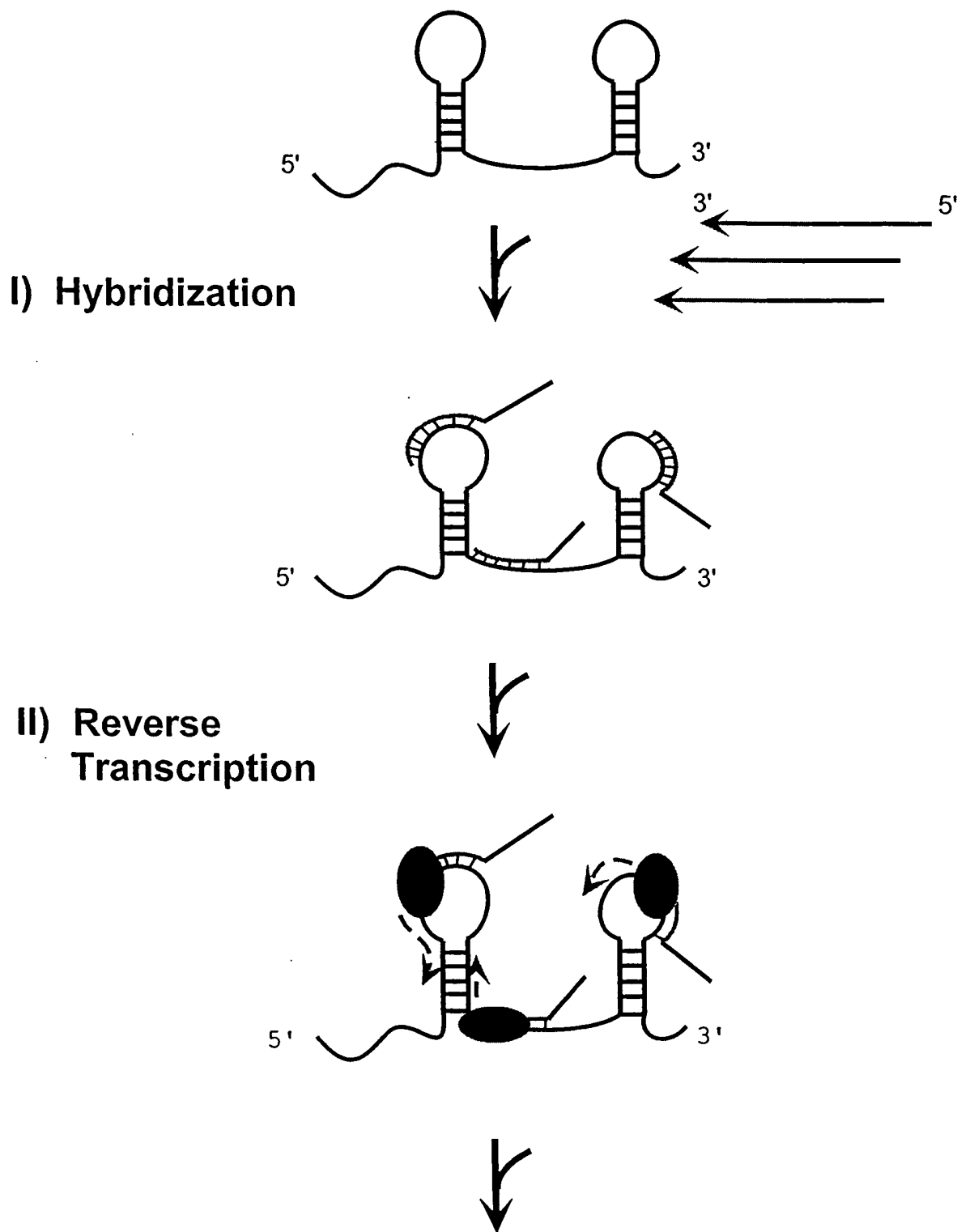


FIGURE 45A

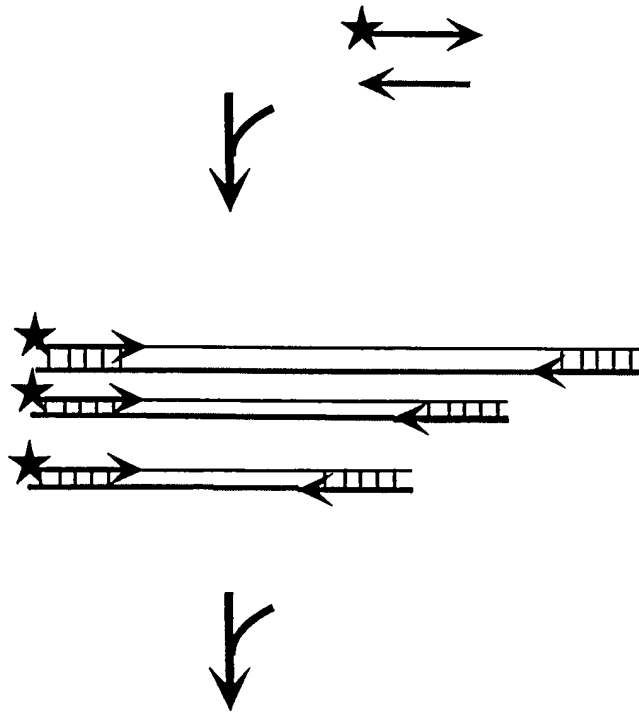
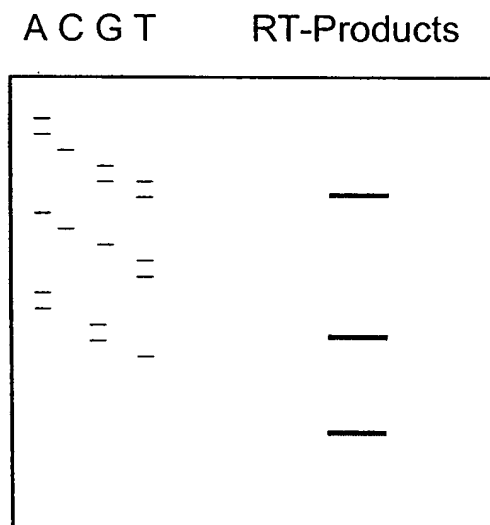
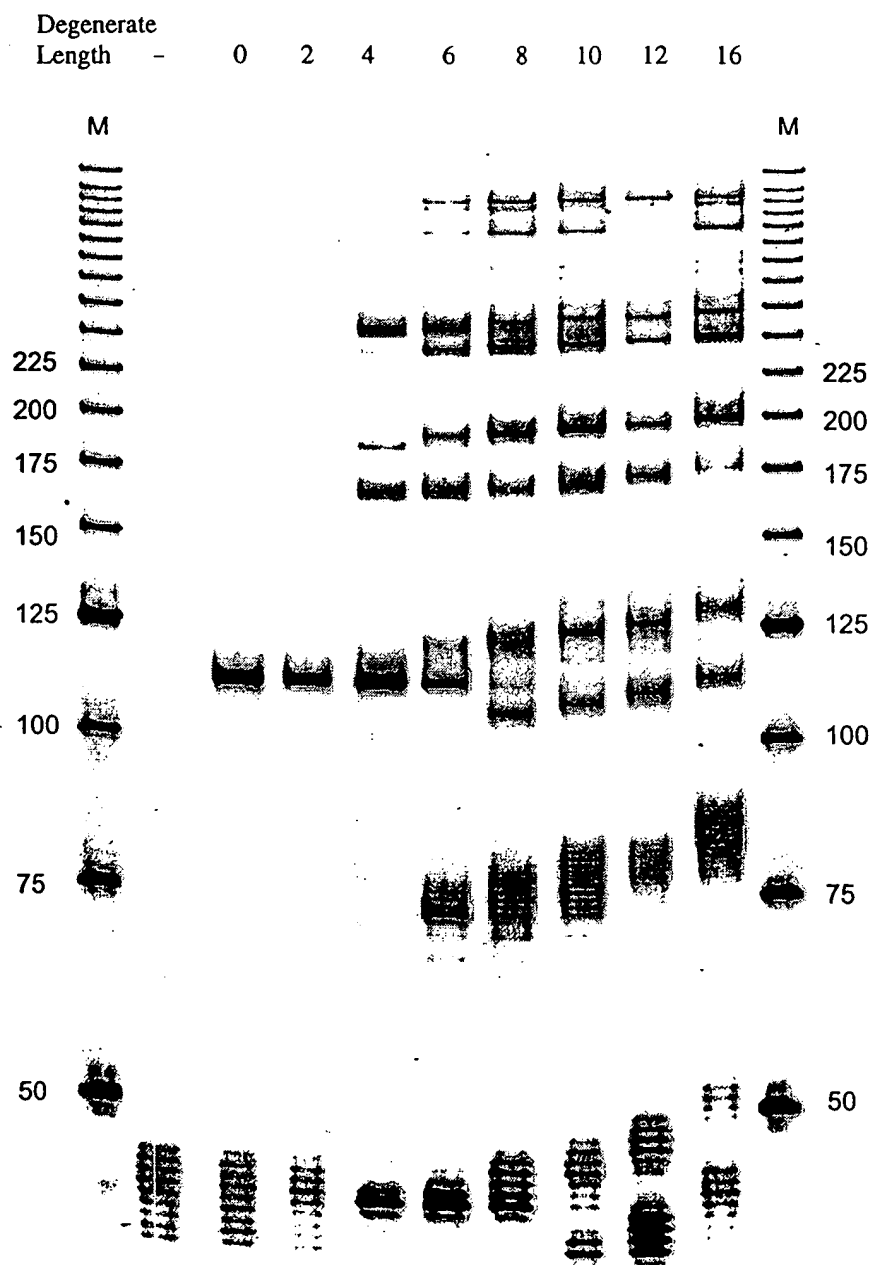
III) PCR**IV) PAGE with Sequencing Ladder****FIGURE 45B**

FIGURE 46



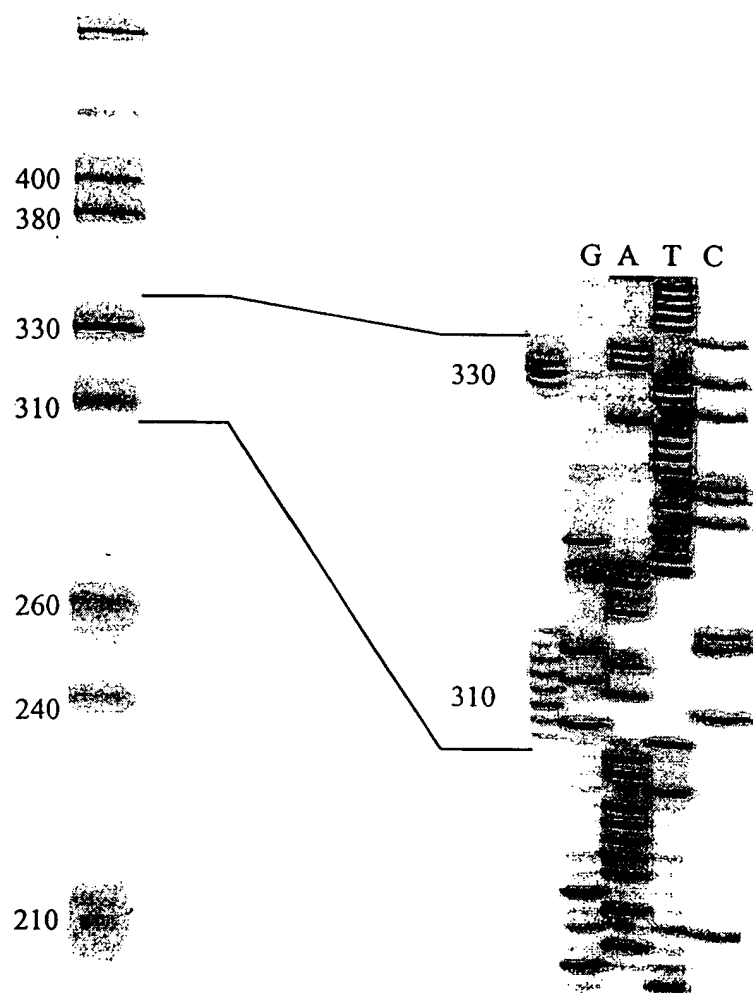


FIGURE 47

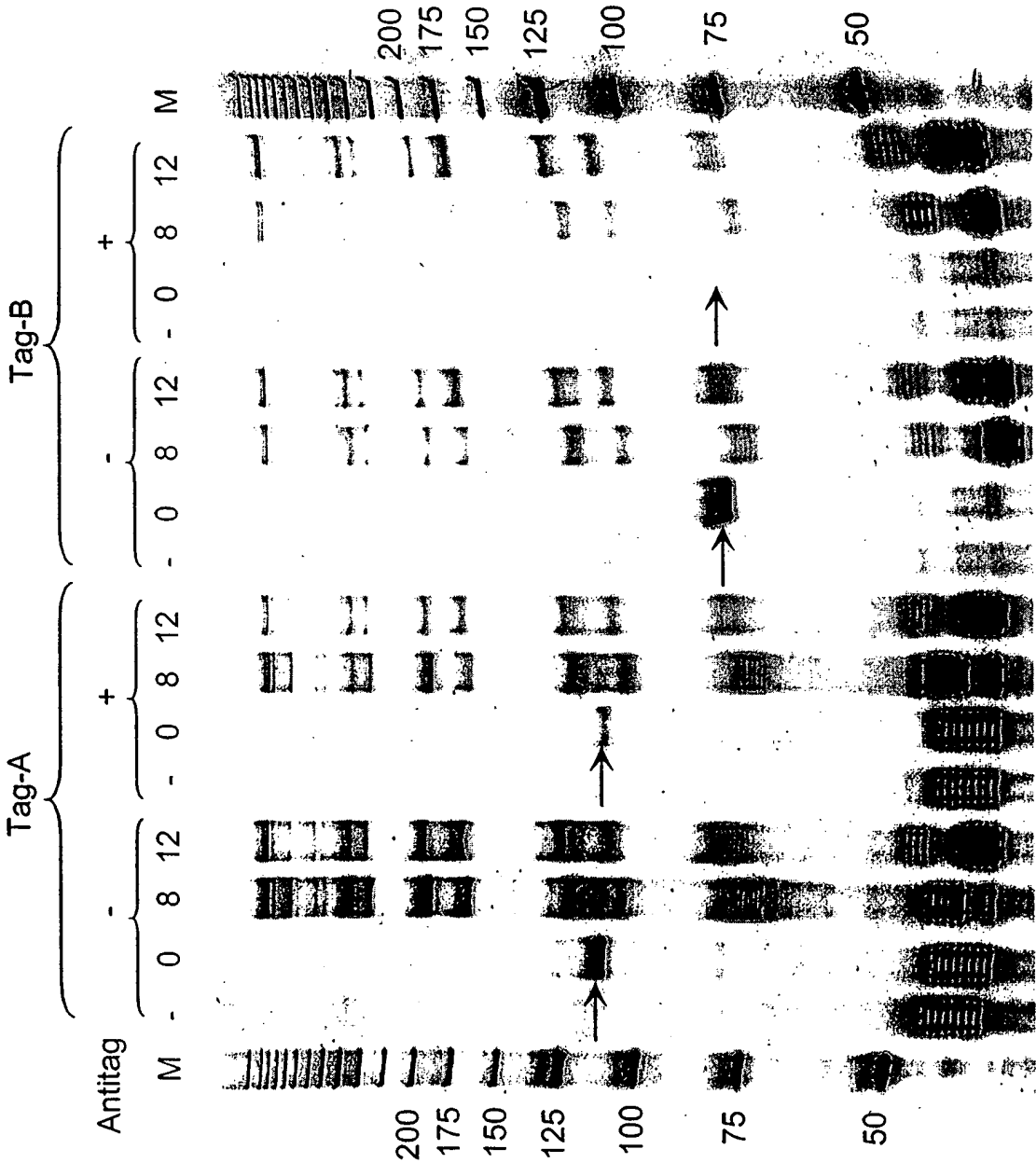


FIGURE 48

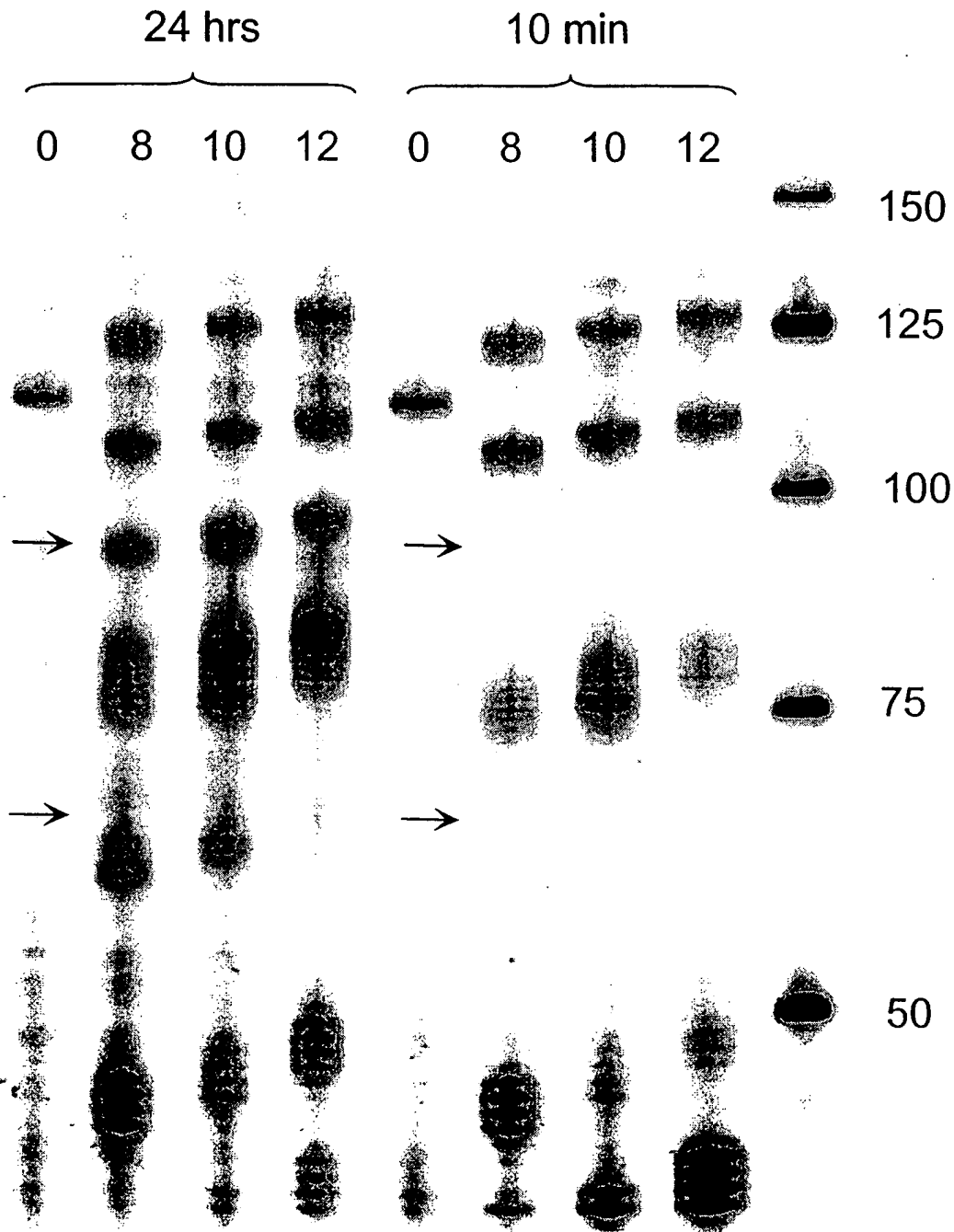


FIGURE 49

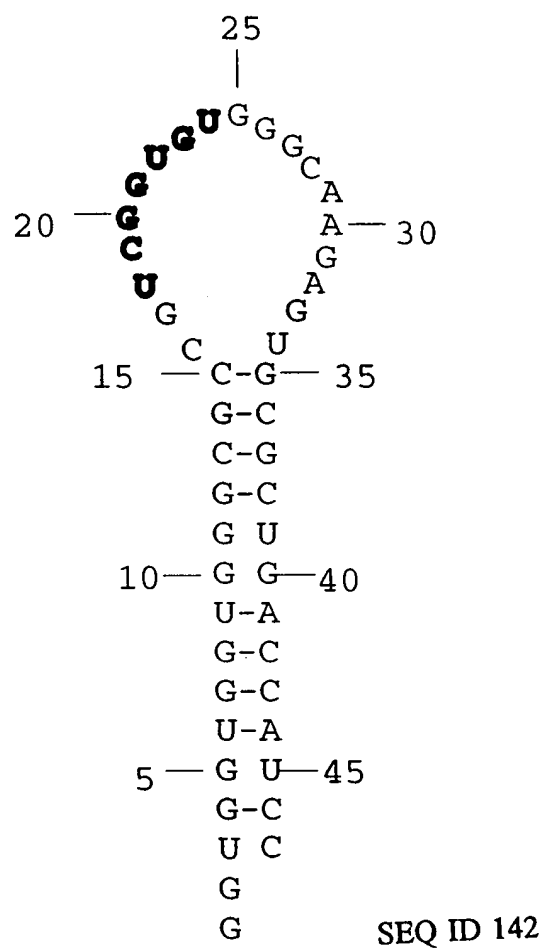


FIGURE 50A

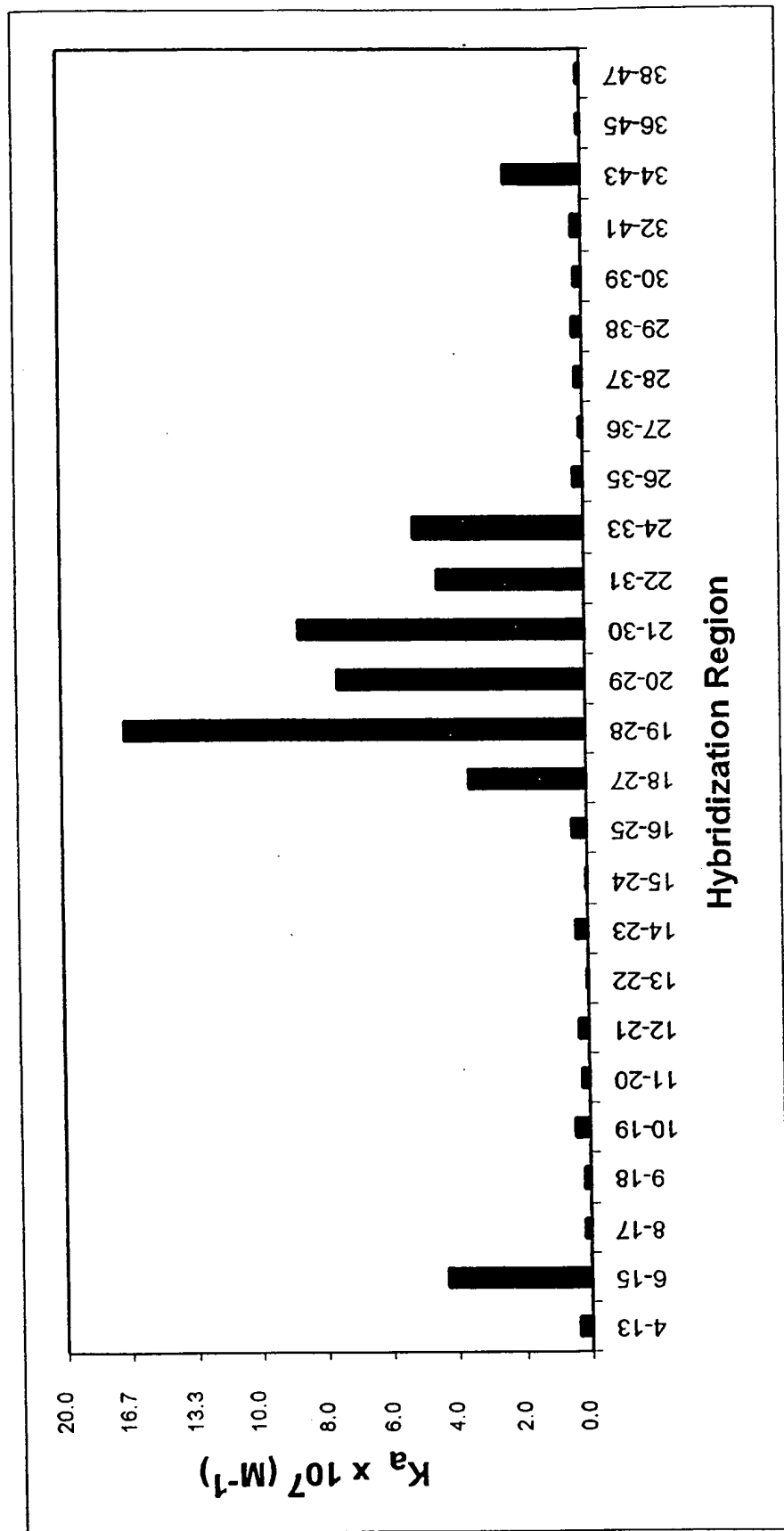


FIGURE 50B

FIGURE 51

1 ACACUUGC UU UUGACACAAC UGUGUUUACU UGC**AAUCCCC** CAAAACAGAC

51 **64-68** AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG UCUGCGGUCA** **88-97** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

FIGURE 52A

ISIS 1571(-) ISIS 3067(+)
1 GCGCCCC AGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570(+)
41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCGGCC
81 CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC
121 CCAGGACCTG GCAATGCCCA GACATCTGTG TCCCCCTCAA
161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG
201 CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG
241 ACCCCGTTGC CTAAAAAGGA GTTGCTCCTG CCTGGGAACA
281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)
321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA
361 ACAGCTAAAA CCTTCCTCAC CGTGTA CTGG ACTCCAGAAC
401 GGGTGGA ACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG
441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA
481 CCCC GGGCCA ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA
as 610
561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA
601 GCCAATTTCT **CGTGCCGCAC** TGA ACTGGAC CTGCGGCCCC
641 AAGGG**CTGGA** GCTGT TTGAG AAC**ACCTCGG** CCCCCTACCA
681 GCTCCAGACC TTTGTC**CTGC** **CAGCGACTCC** CCCACA ACTT
721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG
761 TGGTCTGTTC CCT**TGGACGGG** CTGTTCCCAG TCT**CGGAGGC**
801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC
841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT
881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT
921 GACGTGTGCA GTAATACTGG GGAACCAGAG **CCAGGAGACA**
961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG **GCGCCCAACG**
1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

FIGURE 52C

1041 GACAGTGAAG TGT**GAGGCCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTATG

1241 **GCCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCCG GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTT**TCCC** ACTGCCCATC **GGGGAATCAG** TGA CTGTGCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCTG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CT**GCAGGCCT** **CAGCACGTAC**

FIGURE 52D

1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 AACAGGCCCA AAAAGGGACC CCCATG AAAC CGAACACACA

ISIS 1938 (+)

1641 AGCCACGCCT CCCTGAACCT ATCCCGGGAC AGGGCCTCTT

1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG

1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC ACACCTAAAA

1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA

2041 CAGAAGAAGT GGCCTCCAT AGACATGTGT AGCATCAAAA

FIGURE 52E

ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA **CTGACCCCAA** CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTT**TACCAG** CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAA**AATG**GGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTTC TAT**CGG**CACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCC**AGT**

2441 **GAGG**CCTTAT TCCTCC**CTT**C **CCCC**AAAAC TGACACCTTT

2481 GT**TAGCCACC** **TCCCC**ACCCA CATACATTTT TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGA**ATATG** **CCCA**AGCTAT GCCTTGTCTT CTTGTCCTGT

FIGURE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAU CAGCU AUUAGAAGAG
site 80
 41 AAAGAU CAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC
site 120
 81 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG
 121 GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC
 161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA
site 210
 201 CCCAUAUGUA **CAAGAAGCAG** AAAACCUUAA GAAAUUUUUU
site 240 site 260
 241 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU
 281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG
site 330
 321 AAAAUAAUG **CAGAGCCAAA** UUGUCUCCUU UUACUUCAAA
site 380 site 400
 361 CUUUUUAAAA ACUUUAAAGA UGACCAGAGC AUCCAAAAGA
 401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU
 441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG
 521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC site 560
 561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG site 570
 601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC
 641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUAUUAUA
 681 UUUAACAUA UUUAUAUGGG GAAUAUAUUU UUAGACUCAU
 721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG
 761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUAU UUAUAAUCC
 801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA
 841 CUAUUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA site 850 site 860 site 880
 881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG site 890 site 910
 921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU
 961 AAGUGAAGUG AUACUAUCCA GUUACUA

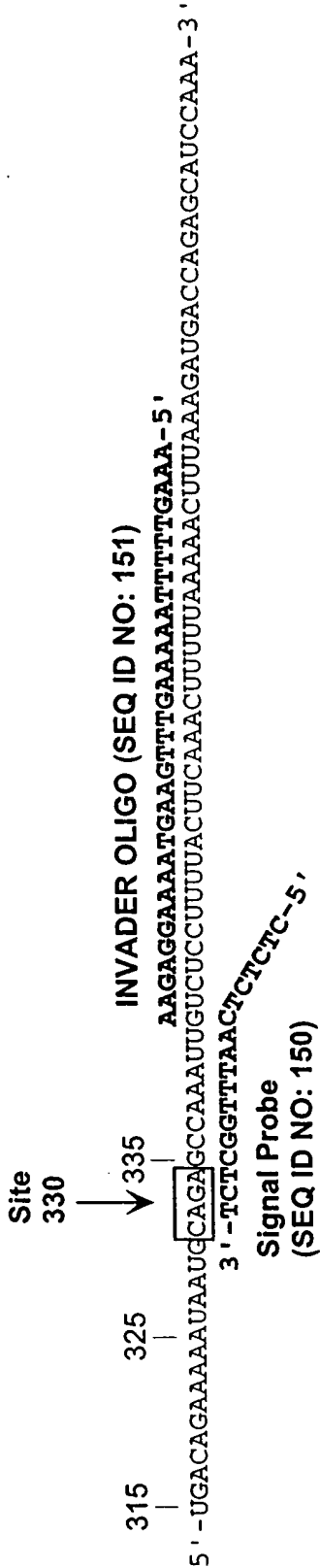


FIGURE 54A

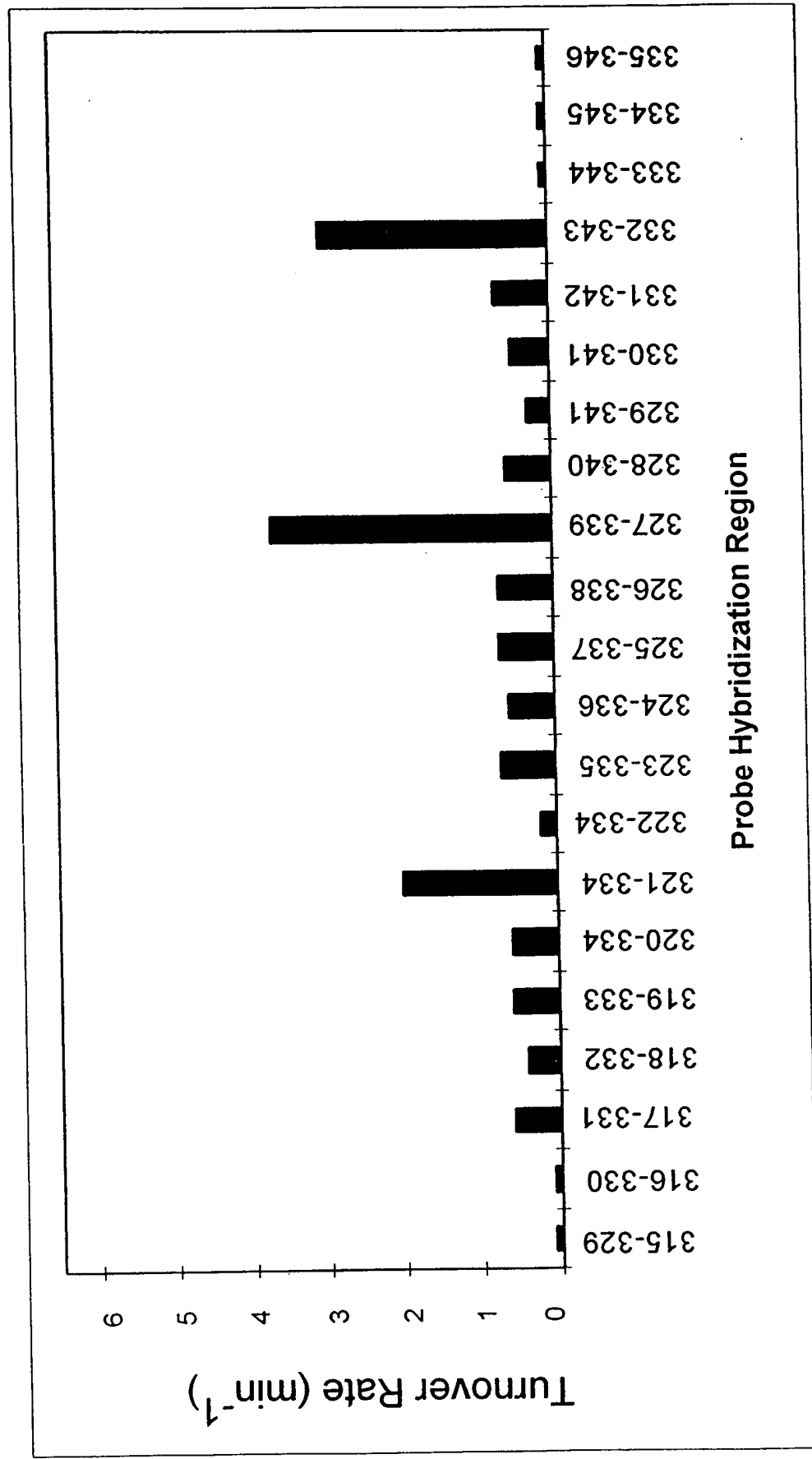


FIGURE 54B

FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC1060 AUCAAAGGAU AGAGAUAAAA GACAC**CAAGG** AAGCUUUAGA CAAGAUAG**AG**

FIGURE 55B

1110 **GAAGAGCAA**A ACAAAGUAA GAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGGACACAGC** AAUCAGGUCA GCCAAAAUUA CCCUAUAGUG CAGAACAUC

Primer 5

1210 **AGGGGCAA**AU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGA**AGGAG** **CCACCCCACA** AGAUUUAAAC ACCAUGCUAA

1360 ACACAGUGGG GGGACAUC**AA** **GCAGCCAUGC** AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUGAGGA**AG CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GGGAAGUGAC** AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUUA UAAAGAUGG AUAUCCUGG GAUUAUUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAGCAAG** CUUC**ACAGGA** GGUAAAAAU **UGGAUGACAG** AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGCGGCUAC** ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGGA

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUA AUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGA**AG** **GGCACACAGC** CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

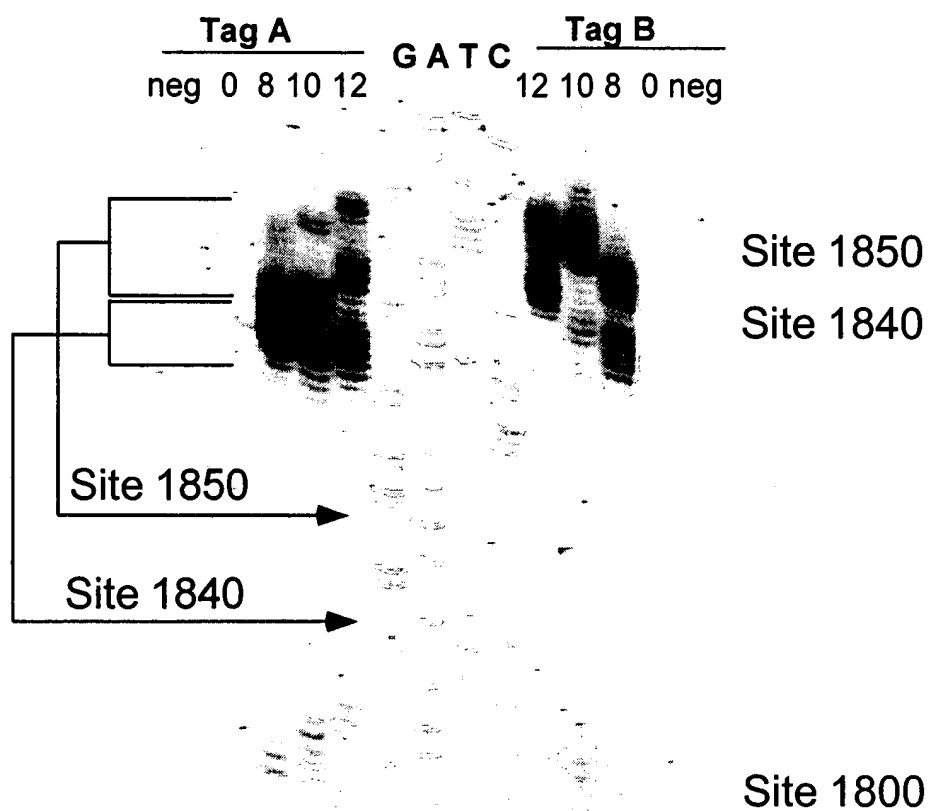


FIGURE 57

(SEQ ID NO:188)	CGTATTCGGTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO:187)	AGGTATTCGGTCTCAAAACCGACT	12
(SEQ ID NO:186)	ACGGTATTCGGTCTCAAAACCGAC	10=11
(SEQ ID NO:185)	CCCGGTATTCGGTCTCAAAACCGA	9
(SEQ ID NO:184)	CGCCGGTATTCGGTCTCAAAACCG	8
(SEQ ID NO:183)	CGCCGGTATTCGGTCTCAAAACCG	7
(SEQ ID NO:182)	AGGCCGGTATTCGGTCTCAAAAC	6
(SEQ ID NO:181)	ATGGCCGGTATTCGGTCTCAAAA	5
(SEQ ID NO:180)	ACTGGCCGGTATTCGGTCTCAAA	4
(SEQ ID NO:179)	ACCTGGCCGGTATTCGGTCTCAA	3
(SEQ ID NO:178)	ATCCTGGCCGGTATTCGGTCTCA	2
(SEQ ID NO:177)	ACTCCTGGCCGGTATTCGGTCTC	1
5'-CAUGCAGGAGUAGGAGGCCCGCCCAUAAAGCAAGUUUGGCUGAAAGCAAUGAG-3'	(SEQ ID NO:158)	
1 CAGTCCCTCATC	(SEQ ID NO:164)	
2 AGTCCCTCATCC	(SEQ ID NO:165)	
3 GTCCCTCATCCT	(SEQ ID NO:166)	
4 TCCCTCATCCTC	(SEQ ID NO:167)	
5 CCTCATCCTCC	(SEQ ID NO:168)	
6 CCTCATCCTCCT	(SEQ ID NO:169)	
7 CTCATCCTCCTG	(SEQ ID NO:170)	
8 TCATCCTCCTGG	(SEQ ID NO:171)	
9 CATCCTCCTGGG	(SEQ ID NO:172)	
10 ATCCTCCTGGGC	(SEQ ID NO:173)	
11 TCCTCCTGGGC	(SEQ ID NO:174)	
12 CCTCCTGGGCC	(SEQ ID NO:175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO:176)	

FIGURE 58

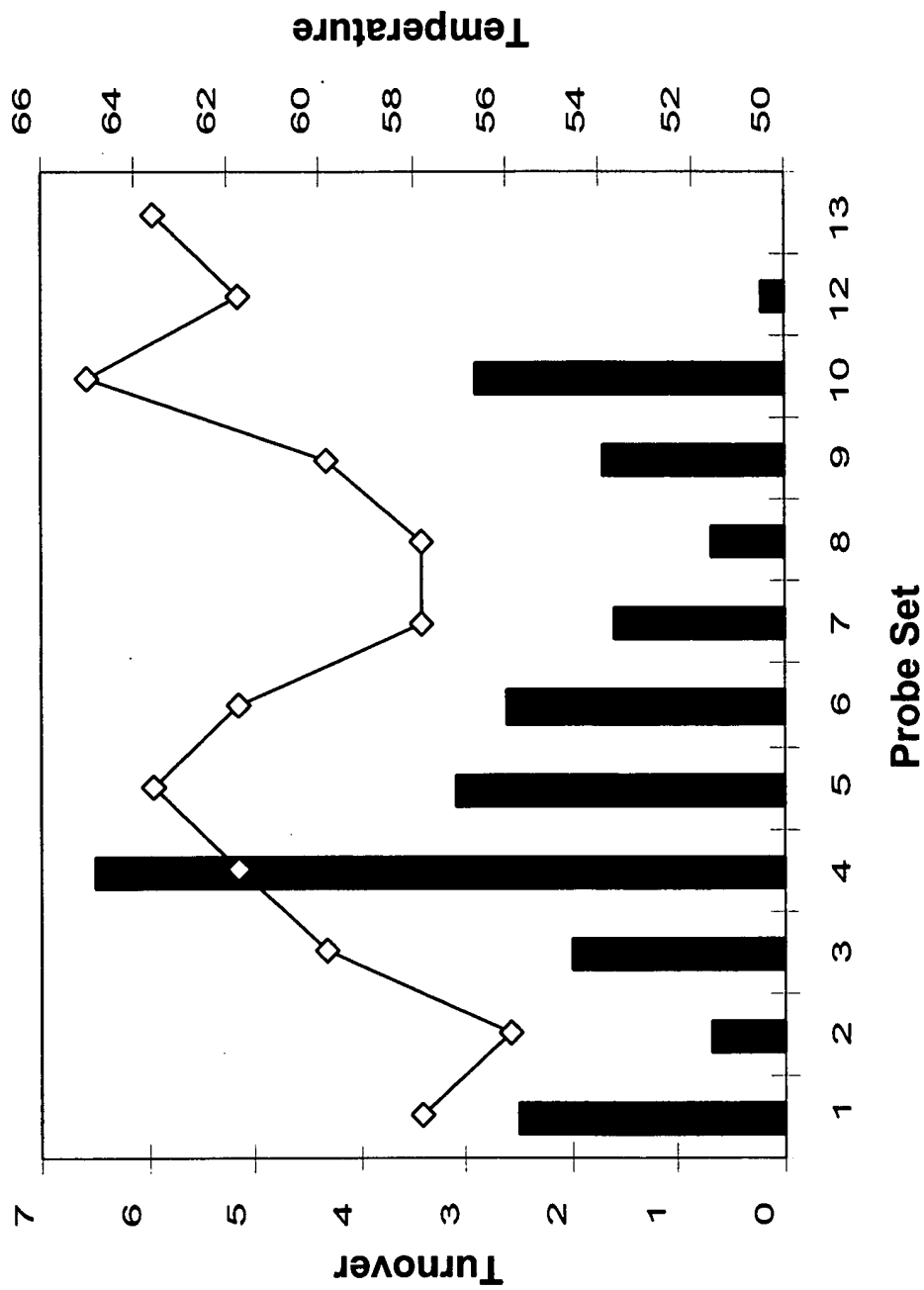


FIGURE 59

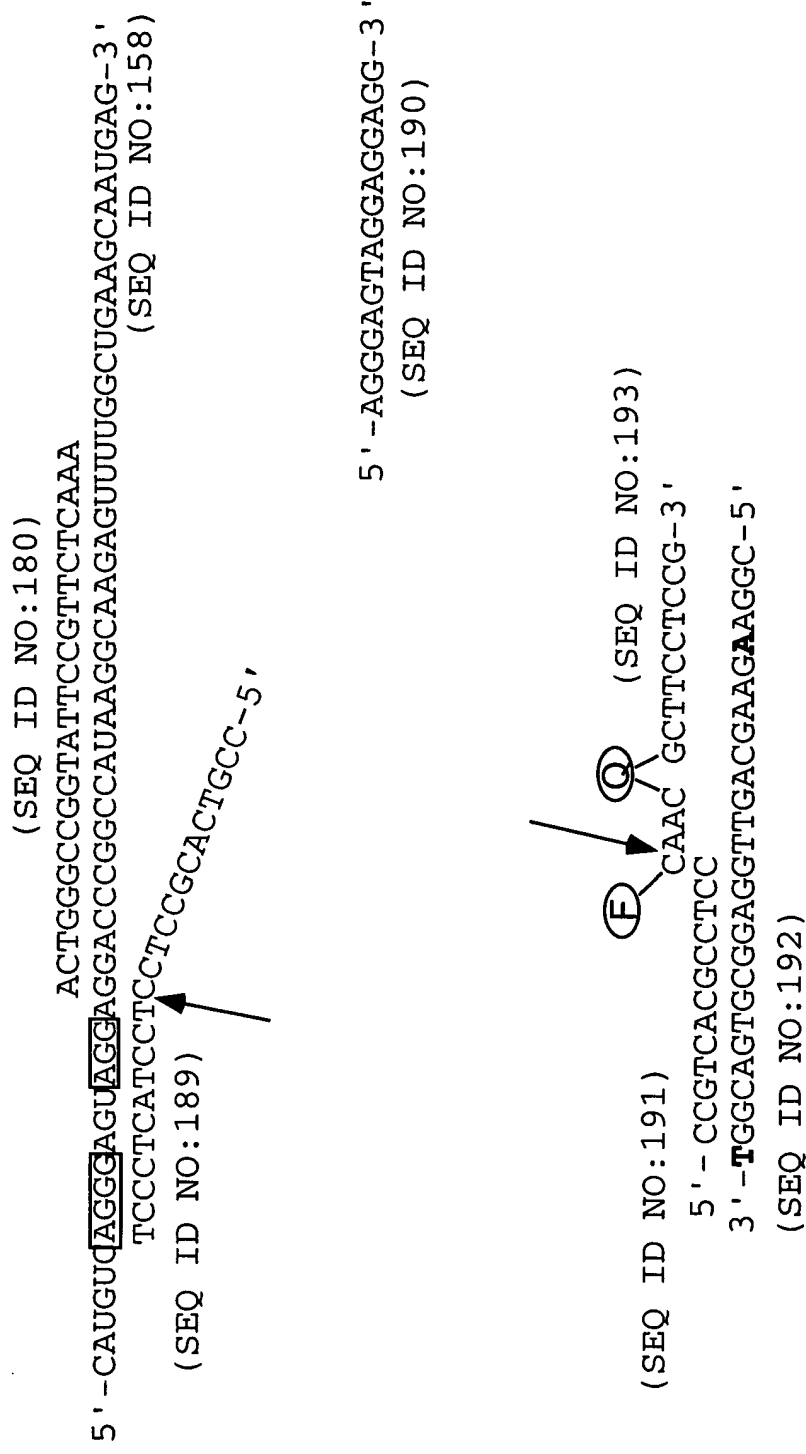


FIGURE 60

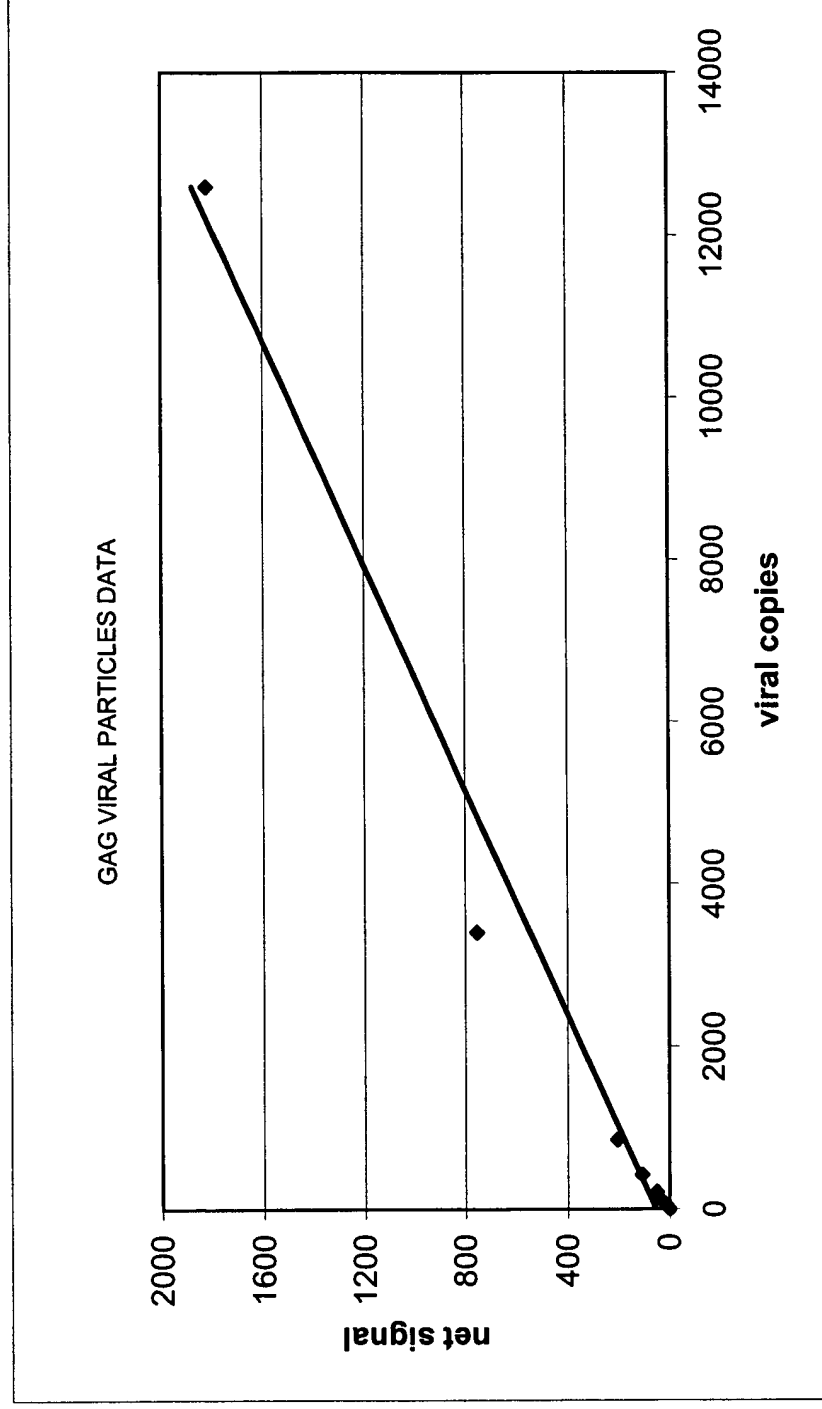


FIGURE 61A

SEQ ID NO:159

primer 1
3300 AGCUGGACUG UCAAUGACAU ACAGAA**GUUA** **GUGGGG**AAAU UG**AAUUGGGC**

3350 AAGUCAGAUU U**ACCCAGGGA** UUA**AAGUAAG** GCAAUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAA**CUGG** CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU

primer 2
3500 GUAUUAUGAC CCAUCAAAAG ACUUAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGGUGCC** CACACUAAUG AUGUAAAACA

3650 AUUAACAG**AG** **GCAGUG**CAAA AAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3
3700 GAAAGACUCC UAAAUUAAA CUGCCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCCU CCCUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGAUG **GGGCAGCUAA** **CAGGGAGACU**

primer 4
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC
 4000 UAGCUUUGCA GGAUUC**CGGGA** UUAGAAGUAA ACAUAGUAAAC AGACUCACAA
 4050 UAUGCAUUAG GAAUCAUUA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU
 primer 5
 4100 AGUCAAUCAA AUAUAG**GAGC** AGUUAUAAA AAAGGAAAAG GUCUAUC**UGG**
 4150 **CAUGGGUACC** AGCACACAAA GGA**AUUGGAG** GAAAUGAACA AGUAGAUAAA
 4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAU**AA**
 4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAU**UGGAGA** GCAAUGGCUA
 primer 6
 4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAU**AGU** **AGCCAGCUGU**
 4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG
 4400 UCCAGGAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC
 4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUAUA U**AGAAGCAGA** AGUUAUUCCA
 primer 7
 4500 GC**AGAAACAG** **GGCAGGAAAC** AGCAUAUUUU CUUUUAAAAU **UAGCAGGAAG**
 4550 **AUGGCCAGUA** AAAACAAUAC AU**ACUGACAA** **UGGCAGCAAU** UUC**ACCGGUG**
 4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

FIGURE 61C

4650 AUUCCCUACA AUCCCCAAG UCA**AAGGAGUA** GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAGGAC AGGUAAGAGA **UCAGGCUGAA** CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAAAGAAUA** GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAAUUUUUC

primer 9

4900 GGGUUUAUUA CAGGGACAGC AGAAAUCCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGAU AUAGUGACAU

5000 AAAA**GUAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

FIGURE 62

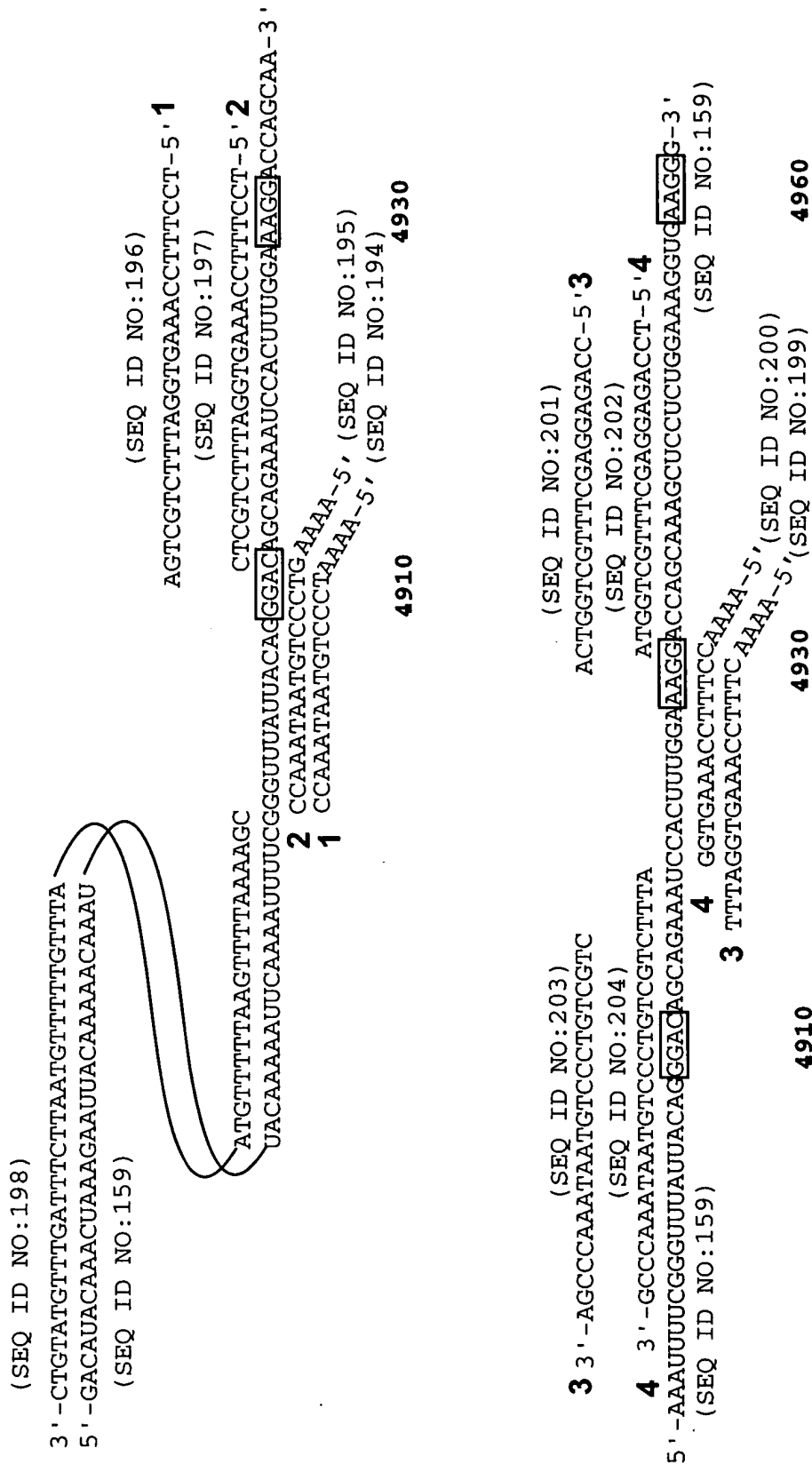


FIGURE 63

(SEQ ID NO:213)
5 3'-TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:209)
ACCCGTCATCATTTATGTTCTATTATCACTGTATTTT-5' **5**
(SEQ ID NO:214)
6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:210)
ACCGTCATCATTTATGTTCTATTATCACTGTATTTTC-5' **6**
5'-GTAAGGACCAGCAAGCUCUCCUGGAAAGGUAAGGEGCAGUAGUAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3'
(SEQ ID NO:159) **5000**
4930 6 CTTTCCACTTCCAAA-5'
5 CCTTTCCACTTCAAAA-5', (SEQ ID NO:206)
4960 (SEQ ID NO:205)

(SEQ ID NO:215)
7 3'-TCGAGGAGACCTTTCCAC (SEQ ID NO:211)
CTCATTATGTTCTATTATCACTGTATTTTCATCACGG-5' **7**
(SEQ ID NO:216)
8 3'-TCGAGGAGACCTTTCCACT (SEQ ID NO:212)
ACATTATGTTCTATTATCACTGTATTTTCATCACGG-5' **8**
5'-GTAAGGACCAGCAAGCUCUCCUGGAAAGGUAAGGEGCAGUAGUAUACAAGAUAAUAGUGACAUAAAAGUAGUGCCAAGAA-3'
(SEQ ID NO:159) **5000**
4930 8 TCCCCGTCATAAAA-5', (SEQ ID NO:208)
7 TTCCCCGTCATAAAA-5', (SEQ ID NO:207)
4960

FIGURE 64

1	4790	(SEQ ID NO:224)	4810	(SEQ ID NO:221)
	3'-TCCCCCTAACCCCCCATG	ATTTCTTATCATCTGTATTATCGTTGCTGTATGT-5'		
	5'-AAGAAAGGGGGGGAAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACU-3'			(SEQ ID NO:159)
		TCACGTCCCCAAAA-5'		(SEQ ID NO:217)
2, 4	4790	(SEQ ID NO:225)	4810	(SEQ ID NO:222)
	3'-CTGTCGTCATGTTTACCGTCATAAGTAGGT	ACCCTAACCCCCCATGTCAC-5'		
	5'-AGACAGCAGUACAAAUUGGCAGUAUUAUCCACAAUUUUAAAGAAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAG-3'			(SEQ ID NO:159)
		GTTAAATTTTCTTTTCCCATAATA-5'		(SEQ ID NO:220)
		GTTAAATTTTCTTTTCCC AAAA-5'		(SEQ ID NO:218)
3	4790	(SEQ ID NO:222)	4810	(SEQ ID NO:223)
	ACCCCTAACCCCCCATGTCAC-5'	CATCATCTGTATTATCGTTGCTGTATGTTGATTTC		
	5'-AAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACUAAAGAA-3'			(SEQ ID NO:159)
		GTCCCCCTTTCTTAAAA-5'		(SEQ ID NO:219)

FIGURE 65

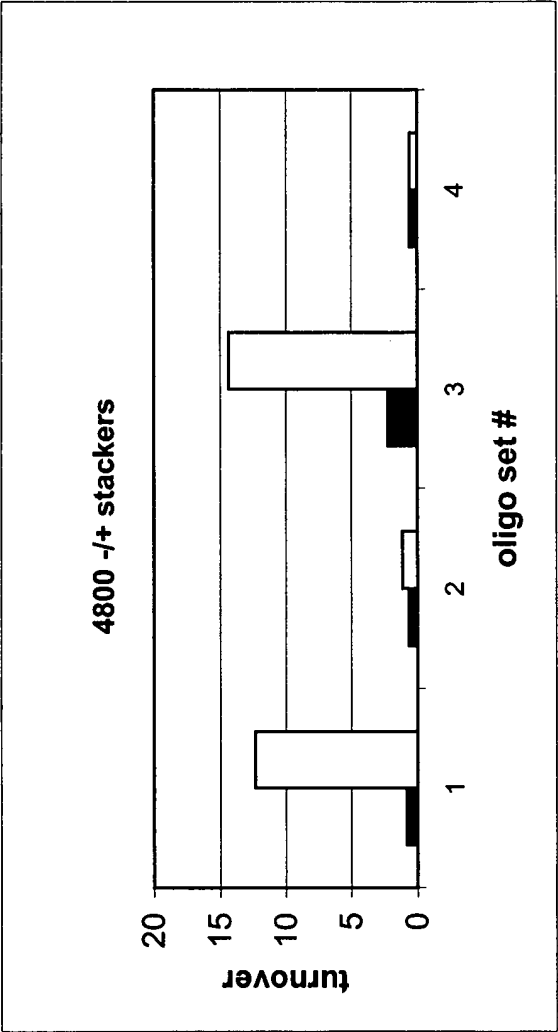


FIGURE 66

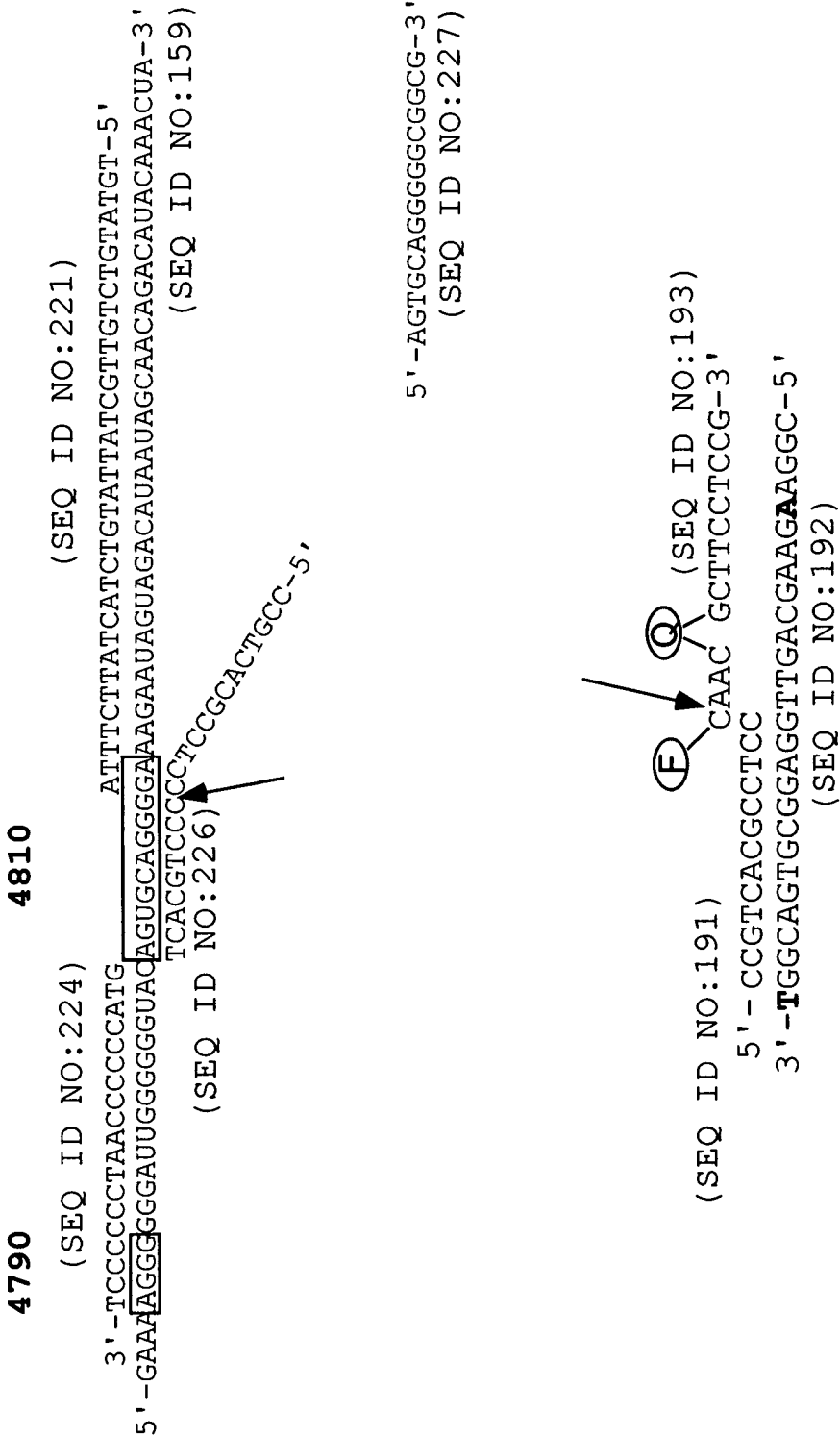


FIGURE 67

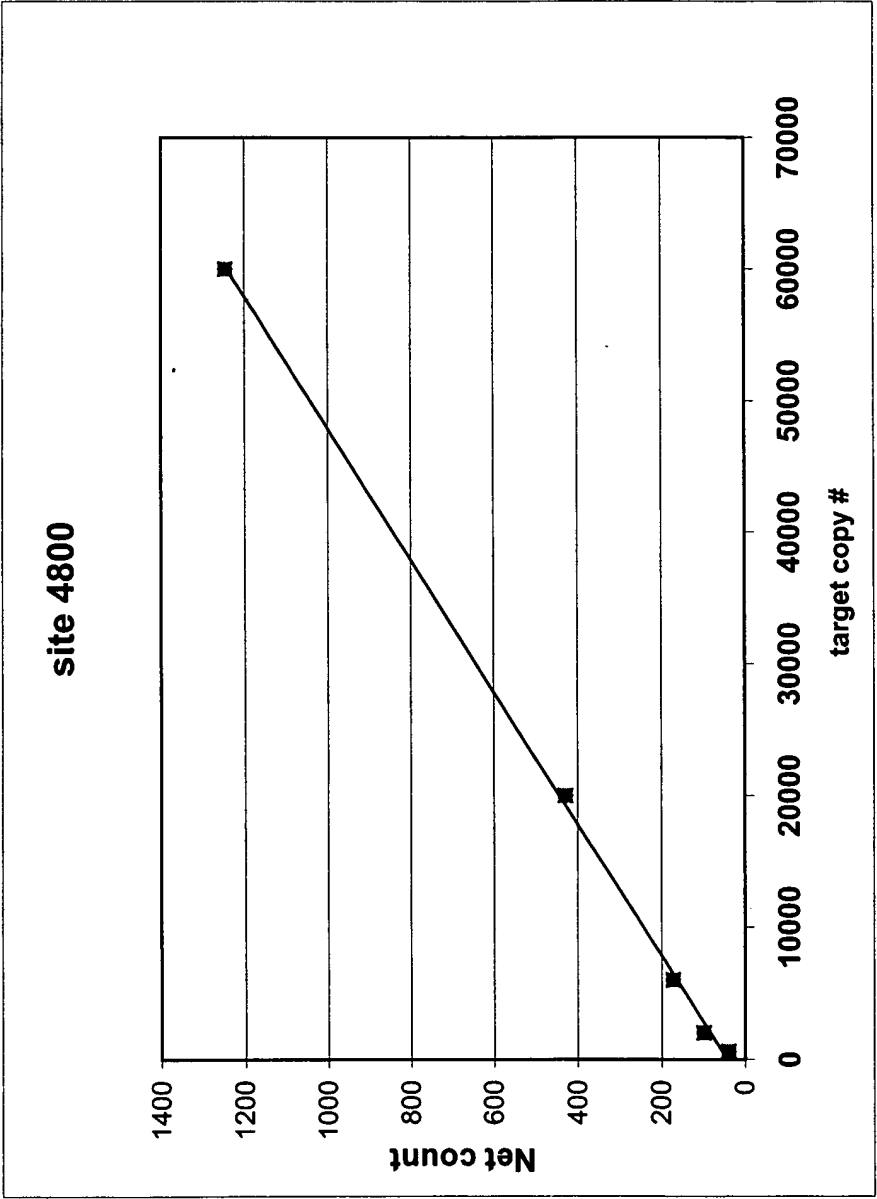


FIGURE 68

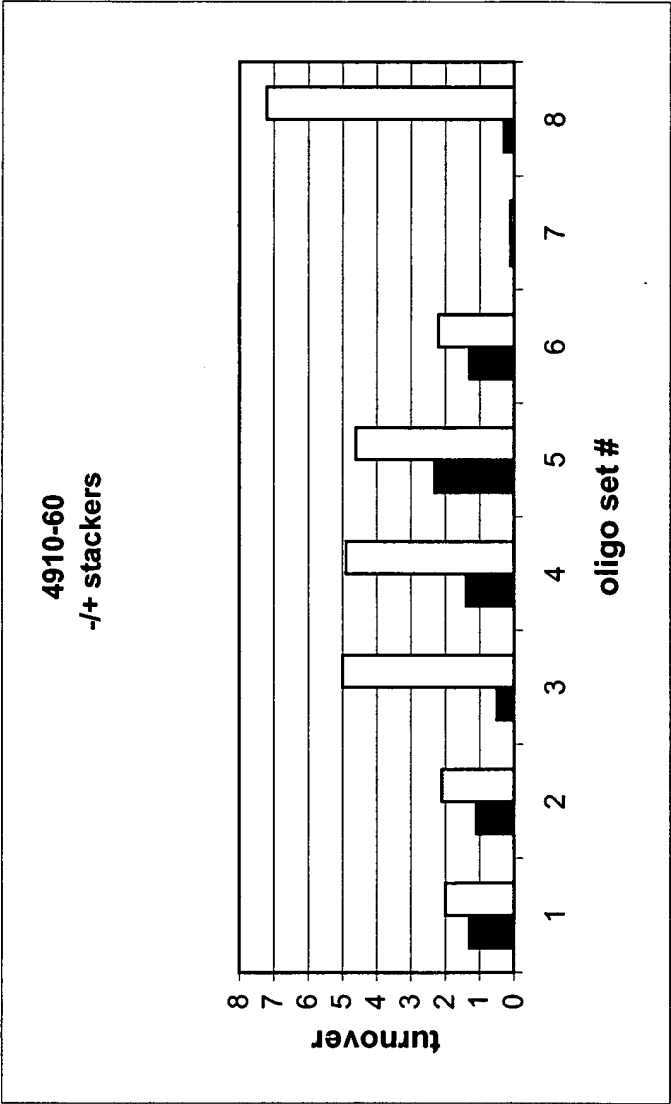


FIGURE 69

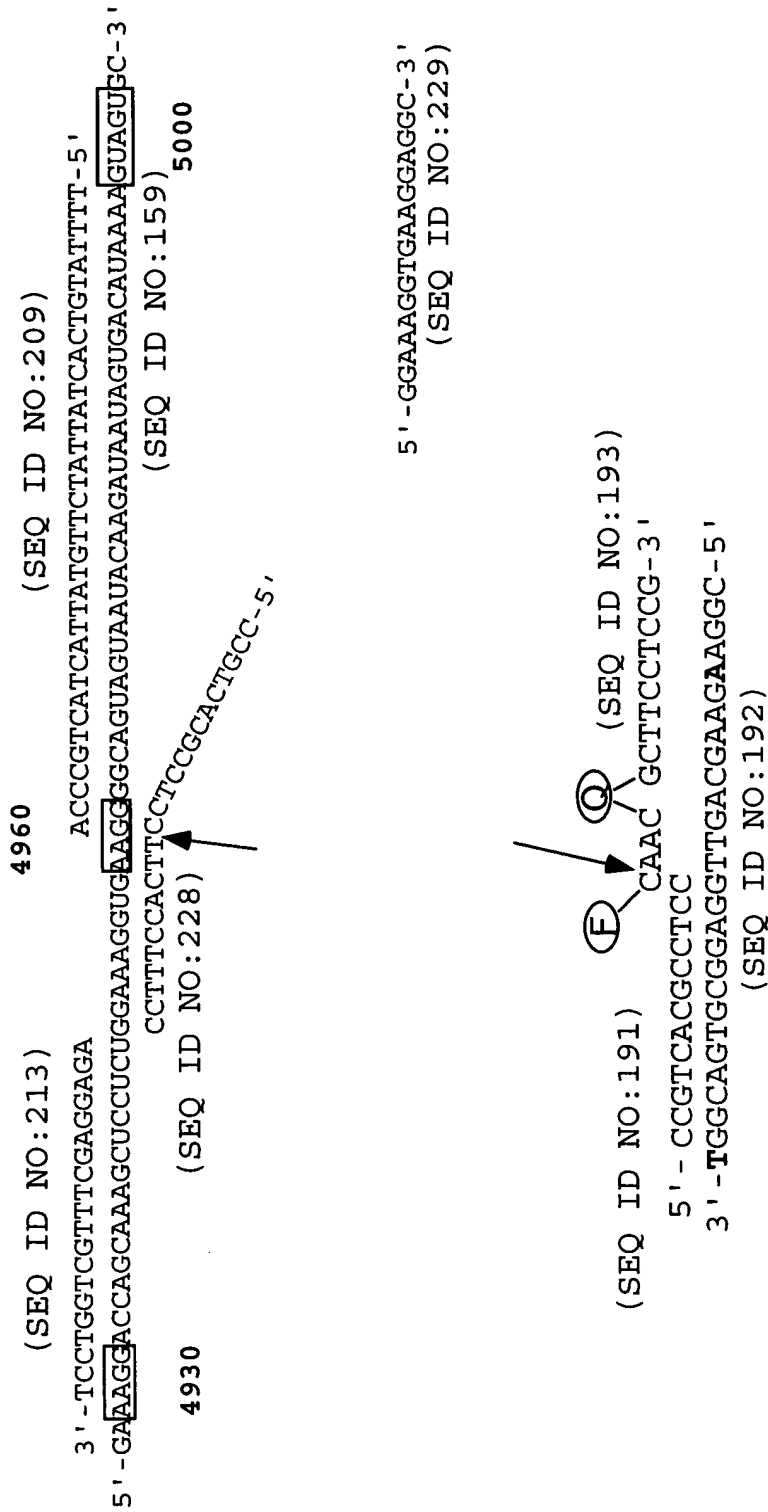


FIGURE 70

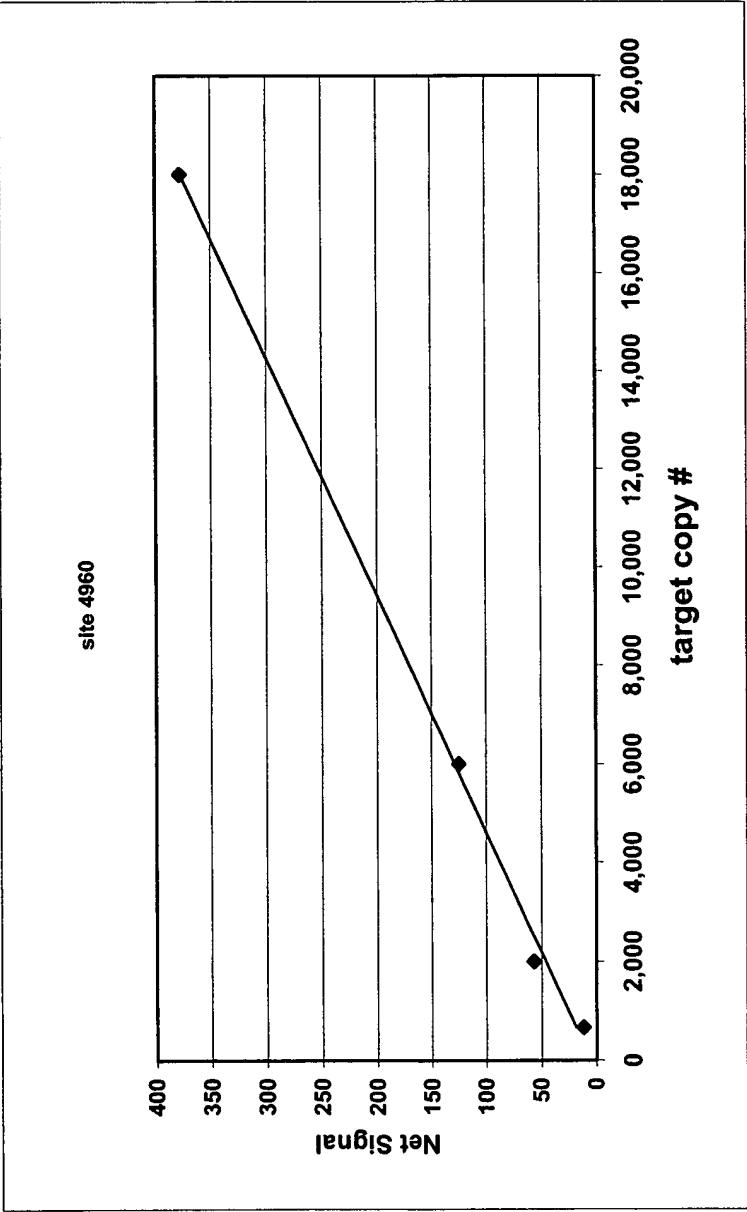


FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUAUGAGGGAGUUC CAGGAGAUUCAACCA
GGAAAUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC
AACUGUGAGACAUGCACUUGCUACGAAACAGAAAUUUCAUGUUGCACCCUUGUUUCUAC
ACCUGUGGGUUAUGACAAAGACAAACUGCCAAAGAAUCUUCAAGAAGGAGGACUGCAAGU
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUCCCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCAAAUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAUGCAGAUUUUCGUGAAAACCCUUA[CGG]GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAUGUA[AAGGC]CAAGAUCCAGGAUAAGGAAGGAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUAUCUUGUGUUGAGACUU[CGUGGUGG]
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA[GCU]GGCUGUCCUGAAAUAUUAUAAGGUGGAUGAGAAUGGCAAAAUUAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUC
UUGGAU[AAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCC]CCGCAAGACUGCU[AGCC]G
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGAGACUGCUAGCCG
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCUCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUCGUGGGGUGACCGGGUCCUUUC
UUGGAA[CAACCC]GCUCAAUACCCAGAAAUUUGGGCGUG[CCCC]CGCGAGAUAC[UAGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aaggggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatctttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAACACUAAUCCACCUCCUGAACAAAGAAAUAUGGGCUGU
GACCGGAAUCUGUGGGCUCAUCGUGGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAUUCUAAUGCCAGUUGGAGACCUGCUUAUCCAGAAGACAAUUAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUAAAACAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUUC
UUCCGAACCUUCACUAUCAGUUGGAAACAGAGGCUGACAACUUCACAGUUCUCAUCUGGC
UGUGGCAGCUGCAUCCCUAUUCUAUCAAUAUCAAUUGUCAAUGAUCCUCAAUUCAC
UUUAUUAACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUUUUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG
UUUUAUCCUUAACAACAUAUCUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA
CAUAAGUAAAGUUGCCAUAAUCGACACUAUAAAGGUAAAAGGAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAAUGGUACAGAUCCAGCCUCAUUUCCACCUUUUGUUGAG
AAAAGCCAGGUAUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCAUCCAAGG
CCUUUGCCUCUCCAGUUGAAAACCAGACAACUAUUGUUUCUGCACAGAAAAAUUAUC
UCAAAAAAUUGUACAUCAUAUGGUGUGCUAGACAUCAGCAAUGCAAAGAAGGGAGACC
UGUGUACAUUUCACUCCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCCCAAUGAAGAAGACAUAGGACAUACUUGGAUUAUCAACCUAUAAUCUG
GAUUCACUUUACA AUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGCAUCAGAA
AAAAUUAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAA

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01 5'-ATGGGGTTTGTAAAGTTG-3' (SEQ ID NO:260)
 761-47-02 5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3' (SEQ ID NO:261)
 937-05-01 5'-TET- atggggtttgttaaagtt-3' (SEQ ID NO:262)
 937-05-02 5'-TET- gaagacgacgagagg-3' (SEQ ID NO:263)
 937-05-03 5'-TET- ggatgatagttcgtgtg-3' (SEQ ID NO:264)
 937-05-04 5'-TET- gctgcagcatattgta-3' (SEQ ID NO:265)
 937-05-05 5'-TET- ctgctatttggatgca-3' (SEQ ID NO:266)
 937-05-06 5'-TET- gcagaagtacatcgga-3' (SEQ ID NO:267)
 937-05-07 5'-TET- gacatgatggaggaga-3' (SEQ ID NO:268)
 937-05-08 5'-TET- agaagaaggatcggg-3' (SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAGUUGUUAAGAAUAAGGC CUACUUUAAGAGAUACCAAGUGAAAUU
 UAGAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAACGCUUGGUGAUACAAG
 AUAAAAUAAAUACAAACACACCCAAAUAACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUUGUCAGAUUGCUUAUGCCC GUUAUAGAGGGGGAUAUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCUGACAAAUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGCUGGCCCGCAGGCUUCUCAAUAGGUUUGGCAUGGACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG
 CCAGGUGCCUUCACCUGCUAUUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
 AGUUUUUGGUGCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCUCACAGUACCA
 AACGAUUCCCGGUUAUGAUUCUGAAAGCAAGGAUUUAAUGCAGAAGUACAUCGGAAG
 CACAUCAUUGGCCAGAAUGUUGCAGAUUACAUGCGCUACUUAAUGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAUAUACAUAAGAACAGCGUAACUCCAGACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUAUGCUGCUAUAACGAGAGAAUCCAGUCUAUGAAAGAAG
 CCCAAGAAAGAAGUUAAAAAGAGAGGUGGAACCGUC CAAAAUGUCCCUUGCUCAGAA
 GAAGGAUCGGGUAGCUCAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA
Oligonucleotides

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caaggggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC
 CCGUCCCUUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC
 AACGGCCAGAAGCCAGUAGU[CCGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
 AAAGGUCAACAUCACCUUCAUGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C
 UCCAUUUCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
 UCUUGGUCCUGGGGGGCUCGAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
 AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
 GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUAUUCUACAACACGUACCUCACAGACAU
 GCUUCCCAUAAAGGGCAAUUGGCCUGUUGUUGGAUGAACAACUCGAAUUC[UGG]GG
 UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
 AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC
 U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
 [CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
 CCCACGUAUUCGUUC[ACGGCC]CCCGAUACUCUGUUGCCAACGGGUCCGUCUACCCACC
 CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
 UGGUGCGCCUCUGUUCUCUCCACCCCCACUUUAC[AACGCCGAC]CCUGUGUUGUCAG
 AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCA[U]
 [CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCA]GC[UGA]GCCUCUACAUCAA
 AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
 GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
 GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
 GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAAUGCUUUUUGUUUUGGA
 GUGGUAGUAAAAAGGGCUCCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCCUGA
 UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
 CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
 CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU
 CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA
 CCAG

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaagagcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcaggtacctggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcatcgtc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaacca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgagggagag-3'	(SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

GGAAGUCCAAGAGCAUCACUGACAUCUUACCUCCUGAACCUGGCCUUGAGCGACCUGCUC
UUUGUGGCCACUUUGCCCUUCUGGACUCACUACCUCAUCAGCCAUGAGGCCUCCACAA
CGCCAUGUGCAAGCUCACGACUGCUUUCUUCUUAUUGGCUUCUUUGGGGGCAUAUUCU
UCAUCACCGUCAUCAGCAUCGACCGGUACCUCGCCAUCGUCCUGGCCGCCAACUCCAUG
AACAACCGGACAGUGCAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGCGGCCAU
CUUAGUGGCGUCGCCCCAGUUCAUGUUCACAAAGAGAAAGGACAACGAAUGUUUGGGUG
AUUACCCCGAGGUCCUGCAGGAAAUCUGGCCCGUGCUCGCAACUCGGAGGUCAACAUC
CUGGGCUUCGUCCUGCCCUGCUUAUCAUGAGCUUUUGCUACUUCCGCAUCGUCCGGAC
GCUGUUUUCUGCAAGAACC~~CGGAAGAAGGCCAGAGCCAUUAGGCUCAUCCUCUUGGUGGU~~
UGUUGUCUUCUCCUCUUCUGGACGCCUUAACAACUUGUGAUUUUCCUGGAGACUCUCA
AAUUCUACAACUUCUCCCUAGUUGUGGCAUGAAGAGGGACCUGAGGUGGGCCCUUAGU
GUGACGGAGACAGUGGCGUUUAGCCACUGCUGCCUCAACCCCUUUAUCUACGCUUUCG
UGGGGAAAAGUUCAGAAGGUACCUGAGACACCUGUACAACAAGUGCCUGGCCGUCCUGU
GCGGUCGUCCUGUCCACGCCGGCUUCUCAACAGAGUCCAGAGGAGCAGGCAGGACAGC
AUUCUGAGCAGCUUGACUCACUACACAAGCGAGGGAGAGGGAUCUCUCCUGCUCUGAAGG
GUCUCCCCGACCCCGACUCUACUAAGAACCCAGAGUCCUGCAUCUGACUCUGUGUAAUG
AAAACAGAUUCACCCCG
CUCCUCCUGCAUUUUAUGUGCAAGAAAUACGGACCAGGUACCUGC

FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-

gtaatttaatacgaactcactataggggaaggtgcagttttgccaaggagtgctaaag-3'

(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatcttatctaataaaacatcat-3'

(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)

781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)

781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)

781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgtacttattaacc-3' (SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)

781-72-02 5'-TET-tgcagttttgccaag-3' (SEQ ID NO:314)

FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUAUGAUGGCUUAUUA CAGUGGCAAUGAGGAUG
ACUUGUUCUUUGAAGCUGAUGGC CCUAAACAGAUGAAGUGCUCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCU CCGACCAC CACUA CAGCAAGGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU C
CCUGCC CACAGACCUUCCAGGAGAAUGA CCUG AGCACCUCUUCUUCUCCUUCUUCUUGAA
GAAGAACCUAUCUUCUUCG ACACAUGG GAU AACGA GGCUUAUGUG CACGA UGCACCUGU
ACGAUC ACUGAACUGCACGCUC CGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCU CUCC ACCUC CAG GGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUGUACAAGGAGAAGAAAGUAAUGACAAAUAACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUAC CUGUCCUGCG UGUUGAAAGAUGAUAAAGCCCACUCUACAGCU
GGAGAGUGUAGAUCCCAAAAUAUACCCAAAGAAGAAGAUGGAAAAGCGAUUUGUCUUCAA
CAAGAUAGAAAUCAAU AACAGCU GGAAUUGAG UCUG CCCAGUUCCCCAACUGGUAC A
UCAGCACCUUCUCAAGCAGAAAA CAUGC CCGUCUUCUGGGAGGGACCAAAG GCGG CCAG
GAUAUAACUGACUUC ACCA UGCAAUUUGUGUCUUCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCC CUAGGGCU GGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA UCAGCCA GGACAGUCAGCUCUCUCCUUU CA
GGCCAAUCC CCAGC CCUUUUGUU GAGCCAGGCCUCUCUCAC CUCUCCUACUCACUU AA
AGCCCGCC UGACAGA AACACGG CCACAUUUGGUUCUAAGAAACCUCUGUCAUUCGU
CCCACAUUCUGAU GAGCAACCGCU UCCCUAUUUUUUUUUUUUUUGUUUGUUUUUA
UUCAUUGGUCUAAUUUAUU CAAAGGGGGC AAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUGGA CUG GUGUGCUCUCUUUAAAUCAAGU
CCUUUAA UUAAGAC UGAAAAUAU AUAAGCU CAGAUUAUUU AAAUG GGAUAUUUAUAA A
UGAGCAAAUAUCAUACUGUUA

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01	5'-TET-GCATCGTTTTGGGTTCTCTT	(SEQ ID NO:316)
448-59-02	5'-TET-ACTTTAAAGATGACCAGAGC	(SEQ ID NO:317)
448-79-01	CACATTGTTCTGATCATCTG	(SEQ ID NO:318)
448-79-02	CGGTAAGTGAATGTC	(SEQ ID NO:319)
448-79-03	TAGTAAGTGAATGTC	(SEQ ID NO:320)
448-79-04	GACATTCAAGTCAGTTACCG	(SEQ ID NO:321)
498-20-01	AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG	(SEQ ID NO:322)
498-20-02	AATTTAATACGACTCACTATACGGTAAGTGAATGTC	(SEQ ID NO:323)
498-20-03	5'-TET-CACATTGTTCTGATCATCTG	(SEQ ID NO:324)
498-20-04	5'-TET-CGGTAAGTGAATGTC	(SEQ ID NO:325)
498-40-01	5'- AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA	(SEQ ID NO:326)
498-40-02	5'- AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC	(SEQ ID NO:327)
498-84-01	5'-TET-CATTCAGATGTAGCG	(SEQ ID NO:328)
498-84-02	5'-TET-GACTCATCAATCAAA	(SEQ ID NO:329)
498-84-03	5'-TET-GATTACAAGGCTTTA	(SEQ ID NO:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCaucUGAAGAUCAGCUAUUAGAAGAGAAAGAUcAGUUAAGUCCUUU
GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUUAACUUCUUUGGCUUAAUUCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUcUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUACUGCCAGGACCCAUAUGUA CAAGAAGCAGAAAACCUUAAGAAAUAU
UUAUUGCAGGUCAUUCAGAUGUAGCGGAUAAUGGAACUCUUUUCUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUcCAGAGCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGAUGACCAGAGCAUC CAAAAGAGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUUCAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGU CGCCAGCAGCUAAAACAGGGAAGCGAAAAAGGAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCCAGUAAUGGUUGUCCUGCCUACAUAUUGAAU
UUUAAAUCUAAAUCUAUUUAUUAUAUAACAUAUUAUUGGGGAUAUAUUUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAUAAGCAACUUUUGUGUAAUGAAAAUGAAUAUCUAU
AAUAUAUGUAUUUAUUUAUAUCCUAUAUCCUGUGACUGUCUCACUAAUCCUUUGUUUU
CUGACUAAUUGGCAAGGCUAUGUGAUUACAAGGCUUUAUCUCAGGGGCCAACUAGGCA
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAUGAAC
ACUUUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAUAAAUUCAGAUUGC
GACACUGUCAAUUGC GGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCCGUGGUAUAGUAAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGGUGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUAUCUGUGGGUGGCCAGCGGCGACUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CAGCGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAAGGUACGUGCCGUCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAAUACCGUUGUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG

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